



1 31
TCG ACT ATG AAT GAT AAT GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61 91
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

121 151 Cadherin
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala
|xx EC motif xx|

181 211
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241 271
AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301 331
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361 391
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421 451
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

481 511
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541 571
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601 631
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661 691
CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG AGT TCT GAC AAA GTC AGT
leu phe ile cys val leu cys phe glu tyr lys gly lys gln ser ser asp lys val ser

721 751
ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781 811
GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA GGG AAC GAC CGA TTT CCA
gly glu gly ala arg gly glu met met arg arg arg ala pro gly asn asp arg phe pro

841 871
GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG
gly leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn glu

FIG. 1 (1 of 5)

901 931
 AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT
 lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

 961 991
 ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT
 thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

 1021 1051
 CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC
 leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn

 1081 1111
 TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC
 cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

 1141 1171
 AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA
 lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

 1201 1231
 GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT
 val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

 1261 1291
 TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA
 tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

 1321 1351
 GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG
 val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

 1381 1411
 AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT
 arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

 1441 1471
 CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA
 pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr

 1501 1531
 GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT
 val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile

 1561 1591
 GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG
 ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu

 1621 |xxxxxxxxxxxxxxxxxxxxxxxx transmembrane domain xxxxxxxx
 AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG
 lys his thr lys lys lys cys tyr thr glu ala ala met cys leu val his ala ala ala

 xxxxxxxxxxxxxxxxxxxxxxxxxxx| 1711
 TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC
 leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val

 1741 1771
 AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG
 ser phe gln asn ile ser ser asn val leu glu glu ser val val ser glu asp thr leu

 1801 1831
 TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC
 ser pro asp glu asp gly val cys ala gly gln tyr phe thr glu ser gly leu val gly

FIG. 1 (2 of 5)

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1861                               1891
CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu

1921                               1951
GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu

1981                               2011
ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met

2041          |xxxxxx ITAM xxxx|          2071
TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln

2101                               2131
GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG
glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu

2161                               2191
GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro

2221                               2251
GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro

2281                               2311
TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu

2341                               2371
CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT
arg arg phe met tyr thr thr pro phe thr leu glu gly arg pro arg gly glu leu his

2401                               2431
GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC
glu gln tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr

2461                               2491          |xxxxxxxxxxxxxxxxxxxxxxxxxxxx
AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA
arg ile ser val ile gln lys glu glu phe val leu thr pro ile glu val ala ile glu

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA
asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|          2611
AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG
lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu

2641                               2671
GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC
glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2701                               2731          |xxxxxxxxxxxx
AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA
asn lys leu arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
AAC AAG CGT CTC ATC ACG GCA CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT
asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys lys asn tyr

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FIG. 1 (3 of 5)

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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX|
AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG
asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys

2881                                2911
CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA
pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

2941                                2971
TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
cys glu thr gln leu ser gln gly ser OCH glu lys pro ser ser phe val glu thr val

3001                                3031
GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG
ala leu gln pro trp arg arg thr cys trp tyr leu lys asn gly thr phe ala thr gln

3061                                3091
GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA
asp STP

3121                                3151
TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG

3181                                3211
GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC

3241                                3271
AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA

3301                                3331
TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA

3361                                3391
AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC

3421                                3451
TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA

3481                                3511
AAA TCA TCA TGG TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA

3541                                3571
ATG GTG GAC TAA TTG CTG TAT AGT TAT TTT TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA

3601                                3631
CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG

3661                                3691
CAG TCA GCC AAA AAT CAC AGA TAC TGC TTT CAC TTA AAT GGA AAC AAT TCT CCG ATA ATG

3721                                3751
CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA

3781                                3811
AGT TTC TTT TTA TAA AGC AAT AAT ATC TCT GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT

3841                                3871
CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT

3901                                3931
TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT

3961                                3991
GTG ACC TTG ACT GAT AAT AAA GAT GTA ATA AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA

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FIG. 1 (4 of 5)

4021
AAC TCG

4021
AAC TCG

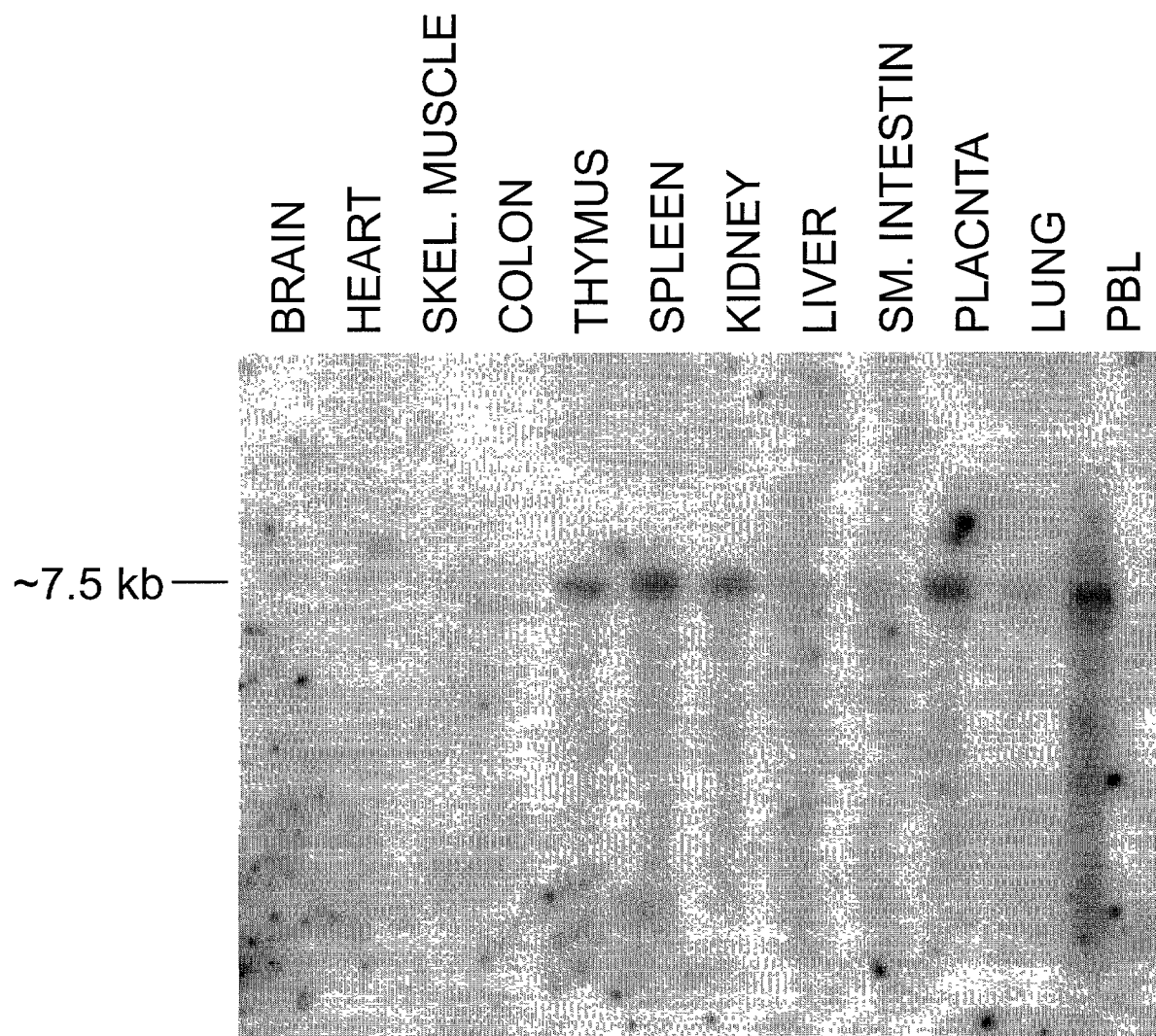


FIG. 2A

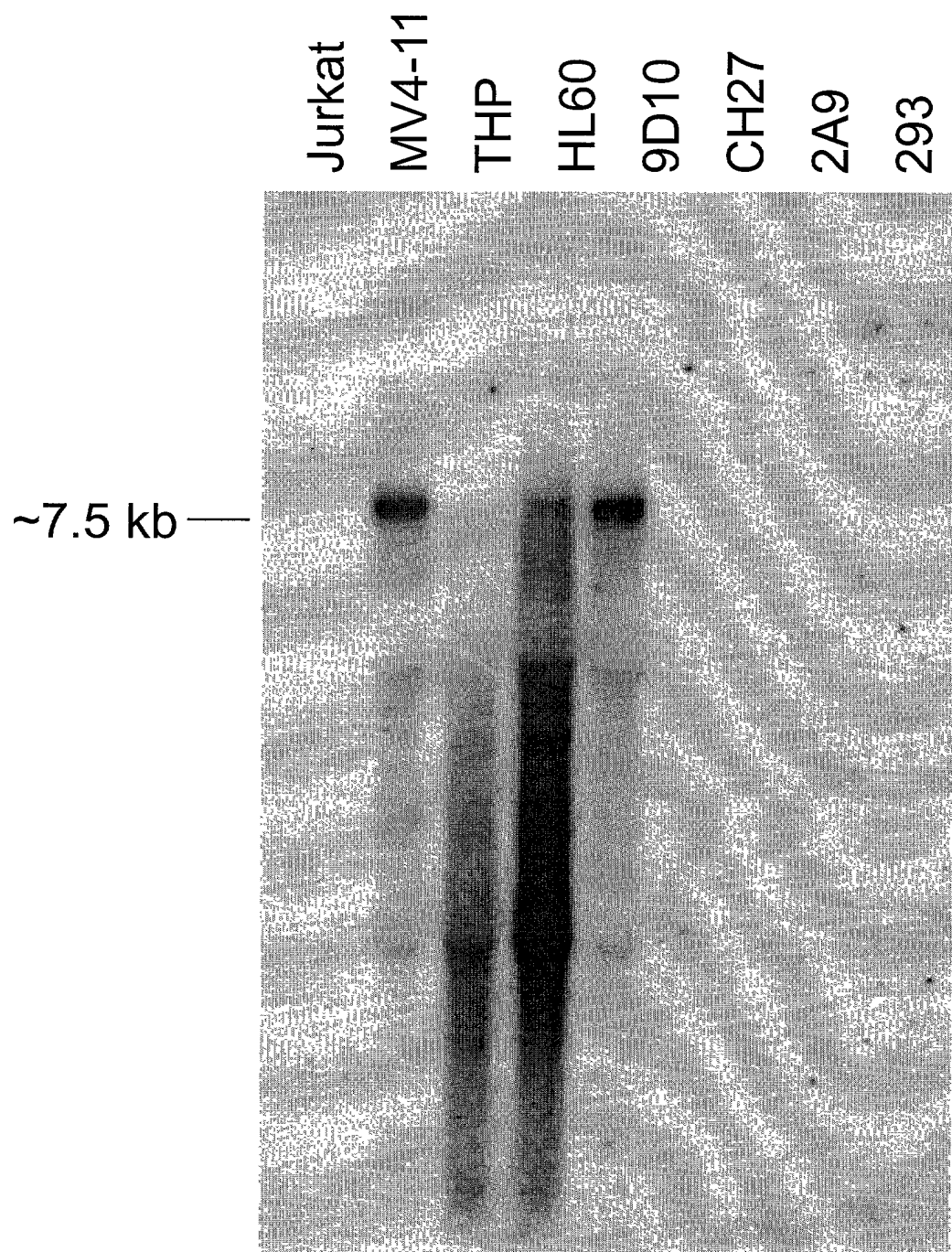


FIG. 2B

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----VLHHHQNPFEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPFEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	PVSANLPSGYLGYPELGMRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA	PVSANLPSGYLGYPELGMRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----

HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLEFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

FIG. 3A (1 of 5)

HC2A I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N
 KIAA I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N
 rat -----
 HC4 L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K P S A P Q A P L I H E T L A T M M I A L L K Q S A D F L A I N
 HC1 L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R --- A C K E R P V H E D L A K N V T G L L K - S N D S P T V K
 HC3 T Q A M D R S C N R M S S H T E T S S F L Q T L T G R L P ---- T K K L F H E E L A L Q W V V C S G -- S V R --- E
 HC5 -----

Cadherin
 Cleavage

HC2A K L L R Y S W F F F D V L I K S M A Q H L I E N S K V K L L R N Q R F P A S Y H H A A E T V V N M L M P H I T Q K F G D
 KIAA K L L K Y S W F F F D V L I K S M A Q H L I E N S K V K L L R N Q R F P A S Y H H A V E T V V N M L M P H I T Q K F R D
 rat -----
 HC4 K L L K Y S W F F F E I I A K S M A T Y L L E E N K I K L T H G Q R F P K A Y H H A L H S L F L A I T - I V E S Q Y A E
 HC1 H V L K H S W F F F A I I L K S M A Q H L I D T N K I Q L P R P Q R F P E S Y Q N E L D N L V M V L S D H V I W K Y K D
 HC3 S A L Q Q A W F F F E L M V K S M V H H L Y F N D K L E A P R K S R F P E R F M D D I A A L V S T I A S D I V S R F Q K
 HC5 -----

HC2A N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S -- C F A P G D P K T L F E Y K F E F L
 KIAA N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S -- C F A P G D P K T L F E Y K F E F L
 rat -----
 HC4 I P K E S R N V N Y S L A S F L K C C L T L M D R G F V F N L I N --- D Y I S -- G F S P K D P K V L A E Y K F E F L
 HC1 A L E E T R R A T H S V A R F L K R C F T F M D R G C V F K M V N --- N Y I S -- M F S S G D L K T L C Q Y K F D F L
 HC3 D T E M V E R L N T S L A F F L N D L L S V M D R G F V F S L I K S C Y Q V S S K L Y S L P N P S V L V S L R L D F L
 HC5 -----

HC2A R V V C N H E H Y I P L N L P M ---- P F G K G R I Q R ----- Y Q D L Q L ---- D Y S L T D E F
 KIAA R V V C N H E H Y I P L N L P M ---- P F G K G R I Q R ----- Y Q D L Q L ---- D Y S L T D E F
 rat -----
 HC4 Q T I C N H E H Y I P L N L P M ---- A F A K P K L Q R ----- V Q D S N L ---- E Y S L S D E Y
 HC1 Q E V C Q H E H F I P L C L P I R S A N I P D L T P S E S ----- T Q E L H A S D M P E Y S V T N E F
 HC3 R I I C S H E H Y V T L N L P C S L L T P P A S P S P S V S S A T S Q S S G F S T N V Q D Q K I A N M F E L S -- V P F
 HC5 ----- M N A D T A P T S P C P S I S --- S Q N S S S C S S F Q D Q K I A S M F D R T S R V P A

Cadherin
 EC motif

HC2A C R N H F L V G I L L R E V G T A L Q E F R E ---- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 KIAA C R N H F L V G I L L R E V G T A L Q E F R E ---- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 rat -----
 HC4 C K H H F L V G I L L R E T S I A L Q D N Y E ---- I R Y T A I S V I K N L L I K H A F D T R Y Q H K N Q Q A K I A Q
 HC1 C R K H F L I G I L L R E V G F A L Q E D Q D ---- V R H L A L A V L K N L M A K H S F D D R Y E R P R K Q A Q I A S
 HC3 R Q Q H Y L A G I V L T E L A V I L D P D A E G L F G L H K K V I N M V H N L L S S H D S D P R Y S D P Q I K A R V A M
 HC5 S S T S - S P G I L F T E L A A A L D A E G E G I S E V Q R K A V S A I H S L L S S H D L D P R C V K P E V K V K I A A

HC2A L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 KIAA L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 rat -----
 HC4 L Y L P F V G L L L E N I Q R L A G R D T L Y S C A A M P N S A S R D E F P C G ---- F T S P -- A N -- R G S L S
 HC1 L Y M P L Y G M L L D N M P R I Y L K D L Y P F T V N T S N Q G S R D D L S T N G G F Q S Q T A I K H A N S V D T S F S
 HC3 L Y L P L I G I I M E T V P Q L Y D F T E T H N Q R G R P I C I A T D D Y E S E ----- S G --- S M I S
 HC5 L Y L P L V G I I L D A L P Q L C D F T V A D T R R Y R --- T S G S D E E Q E ----- G A --- G A I T

FIG. 3A (2 of 5)

HC2A	KDLLGAISGSIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
KIAA	KDLLGAISGSIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
rat	-----
HC4	TDKDTAYGSFQNG-----HGKREDSRGS LIP-EGATGFPDQGNTGEN-----TRQS
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKI PRPL
HC3	QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----
HC5	QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----
HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMDDALFTYWN-KASTSELMDDFFTISEVCL
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMDDALFTYWN-KASTSELMDDFFTISEVCL
rat	-----
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISED TLLTYWN-KVSPQELINILILLEVCL
HC1	ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQNLRLDLLYLCV
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV
HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
KIAA	HQFQYMGKRYIAR-----TGMM
rat	-----
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNSGV
HC1	QNFYRLGKRNIIRKIAAAF--KFVQSTQNNGLKGSNPSCQTSGLLAQWMHSTSRHEGKH
HC3	SCFEYKGKKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
HC5	LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGE GARGEMM
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1	QHRSQTLPIIRGK---NALS NPKL---LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC
HC3	RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNT EKLDKSRAEIEHEALIDGNLATEAN
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH
HC2A	LTALD TSLSLFTLAFKNQLLADHGHNPLMKKVF DVYLCFLQKHQSE TALKNVFTALRSLIY
KIAA	LTALD TSLSLFTLAFKNQLLADHGHNPLMKKVF DVYLCFLQKHQSE TALKNVFTALRSLIY
rat	-----KLSRGHSPLMKKVF DVYLCFLQKHQSE MALKNVFTALRSLIY
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVF DIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1	LTILD TSLSLFTQTHQRQLQQCDCQNSLMKRGFD TYMLFFQV NQSATALKHVFASLRLFVC
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLKVL LHSMACNQSAVYLQHC FATQRALVS
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNC DQSTTYLTHCFATLRALIA
HC2A	KFPSTFYEGRADMC AALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYT GKKS FVRTH
KIAA	KFPSTFYEGRADMC AALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYT GKKS FVRTH
rat	KFPSTFYEGRADMC ALCYEV LKCCNSKLSSIRTEASQLLYFLMRNNFDYT GKKS FVRTH
HC4	KFPSAFFKGRVNMCAAF CYEVLKCCTSKISSRNEASALLYLLMRNNFEYTKRKTF LRTH
HC1	KFPSAFFQGPADLCGSFCYEV LKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3	KFPELLFEEETE QCADLCRLRLRHCS SIGTIRSHPSASLYLLMRQNF EIGN--NFARVK
HC5	KFGDLLFEEEEVEQC FDLCHQV LHHCSSMDVTRS QACATLYLLMRFSFGATS--NFARVK
HC2A	LQVIISVSQ LIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRI RTVLM
KIAA	LQVIISVSQ LIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRI RTVLM
rat	LQVIISLSQ LIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRI RTVLM
HC4	LQIIIAVSQ LIADVALSGGSRFQESLFI INNFANS DRPMLARAFPAEVKDLTKRI RTVLM
HC1	LQLIKAVSQ LIAD-AGIGGSRFQHSLAITNNFANGDKQMKN SNFPAEVKDLTKRI RTVLM
HC3	MQVPMSLSSLVGT SQNFNEEFLRRSLK TILTYAEEDLELRETTFPDQVQDLVFNLHMILS
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMT PFPQTQVEELLCNLNSILY

FIG. 3A (3 of 5)

Transmembrane

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKN	DLSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKN	DLSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKN	DLSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKRWLDSMAKIHVKN	DLSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNG	DLSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPLRLTLWLQNMAKGHSERS	NHAEAAQCLVHS
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQASPLRLTLWLQNMAEKHTKKK	CYTEAMCLVHA

SH3

HC2A	TALVAEYLTRKGV-----	FRQGCTAFRVITPN
KIAA	TALVAEYLTRKEA-----	VQWEPPLPHSHSACLRSSRGGVFRQGCTAFRVITPN
rat	TALVAEYLTRKEAD-----	LALQREPPVPFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEFLHRKKL-----	FPNGCSAFKKITPN
HC1	AALIAEYLKRKGYWKVEKIC	TASLLSEDTHPCDSNSLLTTPSGGSMFSGMWPFLSITPN
HC3	AALVAEYLSMLED-----	RKYLPGVCVTFQNISSN
HC5	AALVAEYLSMLED-----	HSYLPVGSVSFQNISSN

ITAM

HC2A	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLI	IPI
KIAA	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLI	IPI
rat	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP	
HC4	IDEEGAMKEDAGMMD-----	VHYSEEVLELLEQCVNGLWKAERYELI	SEISKLIGPI
HC1	KEEGAAKEDSGMHD-----	TPYNENILVEQLYMCGEFLWKSER	YELIADVKNPIIAV
HC3	VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASF	SMAGMYEAVNEVYKVI	IPI
HC5	VLEESVVSSEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELF	STGGLYETVNEVYKVI	IPI

		ITAM	ITAM		ITAM		ITAM
HC2A	YEKRRD-----						
KIAA	YEKRRDFERLAHL	YDTLHRAYSKV	TEVMHSGRLLGTY	YFRVAFFGQAAQYQ	FTDSETDVE		
rat	SMKSGGTLETHLY	YDTLHRPYSKV	TEVITR-----	A-----	AGSWDLLPGGLFGQ		
HC4	YENRREFENLTQV	YRTHGAYTKI	LEVMTKKRLLG-----		TFERVAFYQG		
HC1	FEKQRDFKKLSDL	YYDIHRSYLVK	VAEVNSEKRLFG-----		RYRVAFYQG		
HC3	HEANRDAKKLSTI	HGKLQEA	FSKIVHQSTG	WERMFG-----	TYFRVGFYG-		
HC5	LEAHREFRKLTL	THSKLQRA	FD	SIVNKDH--KRMFG-----	TYFRVGFFG-		

		ITAM		ITAM	
HC2A	-FFEDEDGKEYIYKEPKLTPLSEISQRL	LLKIYSDKFGSENVKMIQDSGKVNPKDL	DSKYA		
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISQRL	LLKIYSDKFGSENVKMIQDSGKVNPKDL	DSKYA		
rat	GFFEDEDGKEYIYKEPKLTPLSEISQRL	LLKIYSDKFGSENVKMIQDSGKVNPKDL	DSKYA		
HC4	SFFEEDGKEYIYKEPKLTGLSEISLR	LVKLYGEKFGTENVKIIQSDKVNAKEL	DPKYA		
HC1	GFFEEEGKEYIYKEPKLTGLSEISQRL	LLKIYADKFGADNVKIIQDSKNVNPKDL	DPKYA		
HC3	TKFGDLDEQEFVYKEPAITKLAEIS	HRLEGFYGERFGEDVVEVIKDSNPV	DKCKLDPNKA		
HC5	SKFGDLDEQEFVYKEPAITKLPEIS	HRLEAFYQCFGAEFVEVIKDSNPV	DKCKLDPNKA		

ITAM

HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGV	EEQCKRRTILTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGV	EEQCKRRTILTA
rat	YIQVTHVIPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGV	EEQCKRRTILTA
HC4	HIQVTVYVKPYFDDKELTERKTEFERHNISRFVFEAPYTL	SGKKQGCIEEQCKRRTILT
HC1	YIQVTVYVTPFFEEKEIEDRKTD	FEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILT
HC3	YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAH	GELHEQFKRKRTILT
HC5	YIQITFVEPYFDEYEMKDRVITYFEKNFNLRRFMYTTPFTLEGR	PRGELHEQYRRNTVLTT

Y

FIG. 3A (4 of 5)

		Coiled-Coil 1
HC2A	IHCFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
KIAA	IHCFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
rat	IHCFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQGSV
HC4	SNSFPYVKKRIPINCEQQINLKP	TDGATDEIKDKTAEQLKLCSSSTDVDMIQLQLKLQGSV
HC1	SHLFPYVKKRIQVISQSSTELNP	IEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV
HC3	SHAFPIKTRVNVTHKEEIIILTP	IEVAIEDMQKKTQELAFATHQDPADPKMLQMLVQGSV
HC5	MHAFPIKTRISVIQKEEFVLTP	IEVAIEDMKKKTLQLAVAINQEPDAKMLQMLVQGSV
		Coiled-Coil 2
HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAL	LAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAL	LAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAL	LAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLLDSQASKYPKKVSELKDMFRKFIQACSI	ALELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQAL	LDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDAL	RKNKSLIGPVQKE
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEA	VEKNKRLITADQRE
		Coiled-Coil 2
HC2A	YQEEMKANYREMAKELSEIMHE	QICPLEEKTS-VLPNSLHIFNAISGTPPTSTMVHGMTSS
KIAA	YQEEMKANYREMAKELSEIMHE	QLG-----
rat	YQEEMKANYREIRKELSDIIVE	RICPGEDKRATKFPAPHLQRHQRTNKHSGSRVDQFILS
HC4	YHEGLKSNFRDMVKELSDIIEH	QILQEDTMHSPWMSNTLHVFCALSGTSSDRGYGSPRYA
HC1	YQEELRSHYKDLSELSTVMNE	QITGRDDLK---RGVDQTCTRVISKATPALPTVSISS
HC3	YQRELG---KLSS-----	-P-----
HC5	YQQLKKNYNKLNKENLRPMIER	KIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS--
		PBM
HC2A	SSVV-----	
KIAA	-----	
rat	CVTLPHPEPHVGTCFVMCKLRTTFRANHWFCQAQEEAMNGREKEPWT	VI FNSRFYRSWGK
HC4	EV-----	
HC1	SAEV-----	
HC3	-----	
HC5	-----	
HC2A	-----	
KIAA	-----	
rat	VHIFF	
HC4	-----	
HC1	-----	
HC3	-----	
HC5	-----	

FIG. 3A (5 of 5)

	A	B		C		D	E
CLASP-1	YRVAFYGQ:::GFFEEEE	EGKEYIYKEP		PKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFAYIQVTHVTPFFDEKE		RTILTTSHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELN	
KIAA1058	FRVAFFGQAAQYQFTDSETDVEGFFEDE	DGKEYIYKEP		PKLTGLSEISQRLKLYADKFGADNVKIIQDSNKNVNPKDLDPKYAYIQVTVTPFFEEKE		RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELH	
CLASP-2		FEDEDGKEYIYKEP		CLASP-2		RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR	
CLASP-6	FRVAFFGQ:::GFFEDE	DGKEYIYKEP		CLASP-4		RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEV:HDEMSSKKVAELR	
CLASP-4	FRVAFYGQ:::SFFEEEE	DGKEYIYKEP		CLASP-3		RTILTTSNSFPYVKKRIPINCEQQINLKPIDVATDEIKDKTAELO	
DOCK180	FAVGYYGQ:::GFPTFLRGKVFIYRGKEYERRED			KIAA0716		KTILTTSHAFPIYIKTRVNVTHKEEIIILTPIEVAIEDMOKKTQELA	
DOCK2	FAVGYYGQ:::GFPSFLRNKVFIYRGKEYERRED			DOCK3		NTVLTTMHAFPIYIKTRISVIQKEEFVLTPIEVAIEDMOKKTQELA	
DOCK3	FRVGIFYGR:::KFPFFLRNKEYVCRGH			DOCK2		RTSLYLVSPLPGISRWFVEVEKREVVEMSPLENAIEVLENKNQOLK	
KIAA0716	FRVGIFYGK:::KFPFFLRNKEYVCRGH			DOCK180		RTSFVTAYKLPGILRWFEVVMHSQTTISPLENAIETMSTANEKIL	
CLASP-3	FRVGIFYGT:::KFGDLDEQEFVYKEP					RTTTLTLTHSLPGISRWFEVERRELVEVSPLENAIQVVENKNQELR	
CONSENSUS	F V FYG	KEY K		CONSENSUS		RT L FP V + V + P+E AI+ M +L	
	YF	Q F R				F L L + I	

FIG. 3B (1 of 2)

CLASP-1	SLQLKLQGSVSVKVNAGPMAYARAFLEETNAKKYEDNQV--KILKEIFRQFADACGQALD
TRG	KLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KILKEVFRQFVEACGQALA
KIAA1058	KLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KILKEVFRQFVEACGQALA
CLASP-2	KLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KILKEVFRQFVEACGQALA
CLASP-6	KLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KILKEVFRQFVEACGQALA
CLASP-3	MLQMVLGSGVGTTVNQGPLEVAQVFLSE--IPSDPKLFRHHNKLRLCFKDFTKRCEDALR
CLASP-4	QLQLKLQGCVSQVNAGPLAYARAFLLNDSQASKYPPKKVSELKDMFRKFI--QACSIKALE
CLASP-5	MLQMVLGSGVGTATVNQGPLEVAQVFLAE--IPADPKLYRHHNKLRLCFKEFIMRCGEAVE
KIAA0716	PLTMCLNGVIDAAVNGGVSRYQEAFFVKEYILSHPEDGEKIARLRELMLEQAQILEFGLA
DOCK2	PLSMLLNGIVDPAVMGGFAKYEKAFFTTEYYVRDHPEDQDKLTHLKDLIAWQIPFLGAGIK
DOCK3	LLSMCLNGVIDAAVNGGIARYQEAFFDKDYINKHPGDAEKITQLKELMQEQVHVLGVGLA
DOCK180	PLSMLLNGIVDPAVMGGFAKYEKAFFTTEYYVRDHPDAHEKIEKIKDLIAWQIPFLAEGIR
CONSENSUS	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="border: 1px solid black; padding: 2px;">L M L+G V VN G</div> <div style="border: 1px solid black; padding: 2px;">Y AFL + + P</div> <div style="border: 1px solid black; padding: 2px;">L+</div> <div style="border: 1px solid black; padding: 2px;">L</div> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-top: 2px;"> <div style="border: 1px solid black; padding: 2px;">L I</div> <div style="border: 1px solid black; padding: 2px;">V V F +</div> <div style="border: 1px solid black; padding: 2px;">I</div> </div>

DOCK2=KIAA0209
DOCK3=KIAA0299
CLASP2variant=KIAA1058

FIG. 3B (2 of 2)

ref 1.1 ↓

1 31
TCG ACT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61 91
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

121 151
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181 211
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241 271
AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301 331
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361 391
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421 451
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

↓ ref 2.1

481 511
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541 571
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601 631
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661 691
CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG AGT TCT GAC AAA GTC AGT
leu phe ile cys val leu cys phe glu tyr lys gly lys gln ser ser asp lys val ser

721 751
ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781 811
GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA GGG AAC GAC CGA TTT CCA
gly glu gly ala arg gly glu met met arg arg arg ala pro gly asn asp arg phe pro

FIG. 4A (1 of 7)

841 871
GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG
gly leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn glu

901 931
AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT
lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

961 991
ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT
thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

1021 1051
CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC
leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn
↓ ref 3.1

1081 1111
TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC
cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

1141 1171
AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA
lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

1201 1231
GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT
val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

1261 1291
TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA
tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

1321 1351
GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG
val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

1381 1411
AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT
arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

1441 1471
CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA
pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr

1501 1531
GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT
val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile

1561 1591
GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG
ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu

1621 1651
AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG
lys his thr lys lys lys cys tyr thr glu ala ala met cys leu val his ala ala ala

FIG. 4A (2 of 7)

1681	1711
TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG	GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC
leu val ala glu tyr leu ser met leu glu	asp his ser tyr leu pro val gly ser val
1741	1771
AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG	GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG
ser phe gln asn ile ser ser asn val leu	glu glu ser val val ser glu asp thr leu
1801	1831
TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC	CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC
ser pro asp glu asp gly val cys ala gly	gln tyr phe thr glu ser gly leu val gly
1861	1891
CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC	ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu glu gln ala ala glu leu phe ser	thr gly gly leu tyr glu thr val asn glu
1921	1951
GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA	GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu	ala his arg glu phe arg lys leu thr leu
1981	2011
ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC	AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp	ser ile val asn lys asp his lys arg met
2041	2071
TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT	GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe	gly ser lys phe gly asp leu asp glu gln
2101	2131
GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC	AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG
glu phe val tyr lys glu pro ala ile thr	lys leu pro glu ile ser his arg leu glu
2161	2191
GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA	TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
ala phe tyr gly gln cys phe gly ala glu	phe val glu val ile lys asp ser thr pro
2221	2251
GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG	GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
val asp lys thr lys leu asp pro asn lys	ala tyr ile gln ile thr phe val glu pro
2281	2311
TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG	GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
tyr phe asp glu tyr glu met lys asp arg	val thr tyr phe glu lys asn phe asn leu
2341	2371
CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC	CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT
arg arg phe met tyr thr thr pro phe thr	leu glu gly arg pro arg gly glu leu his
2401	2431
GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC	ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC
glu gln tyr arg arg asn thr val leu thr	thr met his ala phe pro tyr ile lys thr
2461	2491
AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT	GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA
arg ile ser val ile gln lys glu glu phe	val leu thr pro ile glu val ala ile glu

FIG. 4A (3 of 7)

2521 2551
 GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA
 asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

2581 2611
 AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG
 lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu

2641 2671
 GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC
 glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2701 2731
 AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA
 asn lys leu arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys

2761 2791
 AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT
 asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys lys asn tyr

2821 2851
 AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG
 asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys

2881 2911
 CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA
 pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

2941 2971
 TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
 cys glu thr gln leu ser gln gly ser OCH

3001 ↓ ref 5.1 3031
 GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG

3061 3091
 GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA

3121 3151
 TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG

3181 3211
 GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC

3241 3271
 AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA

3301 3331
 TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA

3361 3391
 AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC

3421 3451
 TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA

FIG. 4A (4 of 7)

3481	3511
AAA TCA TCA TGG TTG GAA ATT TGG GAG GAG	ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA
3541	3571
ATG GTG GAC TAA TTG CTG TAT AGT TAT TTT	TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA
3601	3631
CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC	ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG
3661	3691
CAG TCA GCC AAA AAT CAC AGA TAC TGC TTT	CAC TTA AAT GGA AAC AAT TCT CCG ATA ATG
3721	3751
CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG	TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA
3781	3811
AGT TTC TTT TTA TAA AGC AAT AAT ATC TCT	GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT
3841	3871
CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT	TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT
3901	3931
TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG	AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT
3961	3991
GTG ACC TTG ACT GAT AAT AAA GAT GTA ATA	AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA
4021	
AAC TCG	

Ref 1.1

Sequence of BAC19 using primer HC5S11, which spans nucleotides 3-22 of the cDNA. Exon sequence is underlined and represents nucleotides 32-57.

CTCTCTGTCTTCATATCTTCCAGGTTATAAAGNATTATTTACTAAAAGAANATTCANGC
TATTTTCATTTAACTAGCTCAGTTTAATCATGTATTTCCCTATAAAGGTTAGTCTTATTAAT
TTGACAAAACAATCAAACAATTCAAACCAGATCAAGTATGCTACCCTGAAGTTACACC
ACTAGCTAAGAATTAACAATCTAAGTAATTGGTTTCTCCCCAGGCTCAAGGCTCCCTGA
TCAGGTTAAGTAAAGCCAAGAATCCAATAAGCCCTATGAAATTTAGAACTCATAGAA
AAGTCTCAAATCTTCTTGTCTGACATTAGCCAATTGTTATATTATGCAAATAGAGGATT
NCAAGTAAATAAGTTTGGAACCTGTTTACCAGGTTTTTGCAGCAGNCCCTCTAAGAGCTT
AACTGGTCATGCATTGAATGCCGAGAGCAAAGAGGAATGGAGAGGGGNTGTAAGNGG
TTCCAATNTTACTGGAACCCACCACTATCTTTNGAAGTCTTGATACTTAACTGNGTGTA
GNCTCTTTAGGCCTNTANTAANTAGAATCTATATGGATTTCGTGTTCTGTCNGCAAGNAG
TGCCTATGAAA

Ref 2.1

Sequence of BAC19 using primer HC5AS10b, which spans nucleotides 560-580 of Exon sequence is underlined and represents nucleotides 510-553.

TGCGAGTAGTGTCGCGTTCAGCATGTTGTACTGCTTATAGGGCTGAAGGGAGGCACG
ATTGGGGGATGGAGGCCAGGGAAGAAGTCAAGCAACAGAAAAATTTGAGGCTTAACA
GTCAAGCAACAGAAAAATTCAAAGTGTCTCTTAAAATACCATGACTGTACATCACTG
CTAGGCTGGAGATCTATTGCCAGTAGCCCTGCCTTCCCTAGGCAGGGGAAGCTGTGTT
CTTTGAGTAGCGCTACTCAGCAAAGAGGCTCACCTGGGGCAGTATTTGAGCTAGGCTT
TCAGCCACCGTATCTGAGTACCTCTGTCTTANGAGCAGTGTGGCCTGGTGATCACCCCT
GGGCCTTGATCATGCGTGCTGCAATCCCAGTGATACAAAGAGGCTTTCATGCTGCTAA
GATCTCCAAGTATTTCTCCTTCGTGCTGGGCAGCAGAGGGTTAGACTTNCAGGGGAGA
AGGAACTGGCTGGGTGCCATGAATAANCTTGCTGTTCAAGANTTAACCTTCTTTGTTAC
ATAAGNGCAAAGGTATAACATAAAGGGNCATGAACTGCTCAACNAAATTNATCAAAT
CCATGTTTGTGGGAGTTCTTTTGTNATNGGAAGTTTAACCCCTAA

Ref 3.1

Sequence of BAC13 using primer C5S3, which spans nucleotides 1086-1105 of the cDNA. Exon sequence is underlined and represents nucleotides 1110-1120.

CCCNGCTCTTTTTGGCAANGTAANCTTGGGATGCTTGTTTTCTTCCTCTTAATTAAGAG
NAAGANTTTTTTTAGCTTCATACTTCTCTCTTCAGGGGGACCAAAAGTCACAGAGCATA
TTAAGTGGCANAAACCCCNAAAGGTCTTAAGTCTTCCTAGGAAGAAAGCAGATGCCCTGA
TTCTGTGGGAAGCCACCATGGAGAGGAAAAGCAGTGGCTCCCATATTTGAAGTGNGGA
CCTAACTCTAGAAAAGTTTAAAANGGCCATTTGCTGAAGGGCTATGACATGAGAACAGA
GATCAACTGAGTGACTTAGCAANTTCACTCTTTCTCTGTAANACCTCTGGTGAGTGAGA
NTAAATCCTNTATGTGACGCCCATTAGTCTTACAAAANGTCATGCCNTAAAATGCCAN
GAAGGNCAGAAATGAATTTCTCACCGCCNGAGGAATGAGGATTATNCTGGGGGGACA
TGCANAAATATTNNCCCCCNATTTATTNATTTATTTATTTTGGAGACNGAGTNTCGNT
CTAATCGCCCCCAGGCTGGNAGGTGGNAGGTGGTTCCCATCTTNAANCTTANNTNGGA
AGGNCCTCTTTGNGCCCCNGGGGGGNGNAAAGNGAATTCCCTAAATGCCTNCANNCCCC
TCCCTGGANGTTATTTGGGGGNNTTNTAAAGGGCNGTGGCNG

Ref 4.1

Sequence of BAC13 using primer C5S7, which spans nucleotides 2196-2205 of the cDNA. . Exon sequence is underlined and represents nucleotides 2225-2231.

ACAAAACTAACCATCANTCTCTAAATCCCAACAANCTTTTTTTAAGAATACCTAANG
AGCTCAACNAGGGGGACTNTCCAANGCACTTAAATGCAGNCAAACNACNCCNNCAAG
AGNGGCAACTACTAATGGGGCANATCTNAAAGAAAATATAGNCAAAGGNNGGAATCA
TAATAGGAGCNACCACTTANGAAGCACCACCTGGGGACCTGGAAGGAGANAGANGGNA
TCTACATACATCATNNNATANCATCCTGCAACGACCCCTGGAAGGAGANAGANGGNA
TTCTTANNNTAGAGANGAGANAACCTGGGGACATGGGAAGAGGNAAGCGAAGGGTTCA
AGGGGANGNAAGCGAGCAGANNCCAGGGNCTCANACTNGNGGGGNNTGGGGGGNTN
CTGNNNCCCTACNCTTNGNANGAACAGNGNNGTTGANNTGGCTTTNGANTA

Ref 5.1

Sequence of BAC13 using primer 122047F1, which spans nucleotides 3537-3556 of the cDNA. Exon sequence is underlined and represents nucleotides 3000-3492.
This region does not contain a intron in this region

FIG. 4A (6 of 7)

CCANNAGATTNTTGNAACGNNGGTAGGCTTCCTTTGTAGATTTATTGAAAATGTTTCGT
ACTTCTACAAGTTTGCCCTGCCTTCCTATAAAGAGTGAAANTCANTTTGAATCGACTGG
TGGATAATTNTTCCATTTTTCTCAGGCAATTTNGAGTTACTCCAATAAATTCAAATAT
GGGCCAGAGGAAATCATCTTTCAGATGGGCAGTGATTGGCCAGTCAGCAGGAGAAGC
TGCTTATGCCTTGTTTGGTACATTGTGGAAAAACACACTTTAATAAATACGCANTCATG
CCTGAGTACCCATCCTCCATCCCGCCACCCCCCAGTATGGCAAAAATCTGGTCAGAGT
CCATTGGAATAATTCCATGGTTCCTGGGATCCCAAAGCTTCCAGAAGTGCTGGCTG
ATCAANGGAGTGTACAGTCAGTCCTGGGTGGCAAAAATGTCCCATTTTTTAAGTACCA
AGCAAAGGTTCTTCTTNCAAGGGTTNCTAGGGCC

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHHLHLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHHLHLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

FIG. 4B (1 of 5)

HC2A IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
 KIAA IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
 rat -----
 HC4 LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
 HC1 LPDIVAKCHEEQLDHSVQSYIKFVKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK
 HC3 TQAMDRSCNRMSSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSG--SVR---E
 HC5 -----

Cadherin
 Cleavage

HC2A KLLRYSWFFFVDVLIKSMAQHLENSKVKLLRNQRFPPASYHHAAETVVNMLMPHITQKFGD
 KIAA KLLKYSWFFFVDVLIKSMAQHLENSKVKLLRNQRFPPASYHHAVETVVNMLMPHITQKFRD
 rat -----
 HC4 KLLKYSWFFFETIAKSMAATYLLLEENKIKLTHGQRFPPKAYHHALHSLFLAIT-IVESQYAE
 HC1 HVLKHSWFFFATILKSMAQHLEIDTNKIQLRPQRFPPESYQNELDNLVMVLSHDHVIWKYKD
 HC3 SALQQAWFFFELMVKSMVHHLYFNDKLEAPKSRFPFERFMDIAALVSTIASDIVSRFQK
 HC5 -----

HC2A NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDHKTLEFYKFEFL
 KIAA NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKLTLEFYKFEFL
 rat -----
 HC4 IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
 HC1 ALEETRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQYKFDL
 HC3 DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPSVIVSLRLDFL
 HC5 -----

HC2A RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF
 KIAA RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF
 rat -----
 HC4 QTICNHEHYIPLNLPM-----AFAKPKLQR-----VQDSNL---EYSLSDEY
 HC1 QEVCQHEHFIPCLPIRSANIPDLTPSES-----TQELHASDMPESYVTNEF
 HC3 RIICSHHEHYVTNLPCSLTTPASPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF
 HC5 -----MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA

1.1

Cadherin
 EC motif

HC2A CRNHFLVGILLREVGTALEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
 KIAA CRNHFLVGILLREVGTALEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
 rat -----
 HC4 CKHHFLVGILLRETSIALQDNYE---IRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQ
 HC1 CRKHFLIGILLREVGTALEQEDQD---VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS
 HC3 RQQHYLAGIVLTELAVILDPDAEGLFGLHKKVINMVHNLSSHSDSDPRYSDPQIKARVAM
 HC5 SSTSSPGLLFTELAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPKVCVPEVKVIAA

HC2A LYLPLFGLLIENVRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
 KIAA LYLPLFGLLIENVRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
 rat -----
 HC4 LYLFPVGLLLENIQRLAGRTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
 HC1 LYMPLYGMLLDNMPRIYKLDLYPTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTSFS
 HC3 LYLPLIGIIMETVPQLYDFTETHNQRGPICIAATDDYESE-----SG---SMIS
 HC5 LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT

FIG. 4B (2 of 5)

		Refs
HC2A	KDLLGAISGIA SPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS	
KIAA	KDLLGAISGIA SPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS	
rat	-----	
HC4	TDKDTAYGSFQNG-----HGIKREDSRGS LIP-EGATGFPDQNGTGEN-----TRQS	
HC1	KDVLNSIA AFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL	
HC3	QTVAMAIAGTSVPQ-----LTRPGSFLLT STSGRQHT-----	2.1
HC5	QNALAIAGNNFN-----LKTSG-IVLSS LPYKQYN-----	
HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL	
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL	
rat	-----	
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLTYWN-KVSPQELINILILEVCL	
HC1	ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSIIPVCL	
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLDLLYLVCV	
HC5	-----MLNADTTNRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV	
HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM	
KIAA	HQFQYMGKRYIAR-----TGMM	
rat	-----	
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNSGVM	
HC1	QNFRLGKRNIIRKIAAAF--KFVQSTQNNGTGKSNPSCQTSGLLAQWMHSTSRHEGK	
HC3	SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV	
HC5	LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEGARGEMM	
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
rat	-----	
HC4	QARLQHL-----SSLESS-----FTLNHSTTTEADIFHQALLEGNTATEVS	
HC1	QHRSQLPIIRGK---NALS NPKL----LQMLDNTMTS NSNEIDIVHHVDTEANIATEGC	
HC3	RRSRGQ ERSPSGS AFGSQENLRWRKDMTHWRQNT EKLDKSRAEIEHEALIDGNLATEAN	
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH	
HC2A	LTALDTLSLFTLAFK NQLLADHGHNPLMKKVFDVYLCFLQKHQSE TALKNVFTALRS LIY	
KIAA	LTALDTLSLFTLAFK NQLLADHGHNPLMKKVFDVYLCFLQKHQSE TALKNVFTALRS LIY	
rat	-----KLSRGHSPLMKKVFDVYLCFLQKHQSE MA KNVFTALRS LIY	
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS	
HC1	LTILDVSLFTQTHQRQLQQCDQNSLMKRGFDTYMLFFQVQNSATALKHVFASLRLFVC	
HC3	LIILDTLEIVQTVS--VTES--KESILGGVLKVLHSMACNQSAVYLQHC FATQ RALVS	
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDQSTTYLTHCFA TLRALIA	3.1
HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
HC4	KFP SAFFKGRVNMCAAF CYEVLKCC TSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTH	
HC1	KFP SAFFQGPADLCGSFCYEVLKCCNHR SRSTQTEASALLYL FM RKNFEFNKQKSIVRSH	
HC3	K FPELLFEEETE QCADLCLRLLRHCSS IGTIRSHPSASLYLLMRQ NFEIGN--NFARVK	
HC5	KFGDLLFEEVE QC FDLCHQVLHHCSS MDVTRSQACATLYLLMRFSFGATS--NFARVK	
HC2A	LQV IISVSQ LIADVVIGIGTRFQ QSL SIINNCANS DR L IKHTSFSSDV KDLTKR IRT VL M	
KIAA	LQV IISVSQ LIADVVIGIGTRFQ QSL SIINNCANS DR L IKHTSFSSDV KDLTKR IRT VL M	
rat	LQV IISVSQ LIADVVIGIGTRFQ QSL SIINNCANS DR L IKHTSFSSDV KDLTKR IRT VL M	
HC4	LQ IIIVS Q LIADVALSGGS RFQES FIINNFANS DR PMLARAFPAEV KDLTKR IRT VL M	
HC1	LQ L IKAVS Q LIAD-AGIGGS RFQ HS L AITNNFANGDK Q MKN BNFPAEV KDLTKR IRT VL M	
HC3	MQV PMSLSS LVGTSQNFNEEFLRRSLK ILT YAEEDLE RETTF PDQVQD LVFN L M ILS	
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMT PFPTQVE ELL CN LS ILY	

FIG. 4B (3 of 5)

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN	DLSEAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN	DLSEAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN	DLSEAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD MAKIHVKN	DLSEAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESM AKIHARNG	DLSEAMCYIHI
HC3	DTVKMKEHQEDPEMLIDL MYRIAKGYQTS PDLRLTWLQNMAGKHSERS	NHAEAAQCLVHS
HC5	DTVKMREFQEDPEMLMDL MYRIAKSYQAS PDLRLTWLQNMAEKHTKKK	CYTEAAMCLVHA

SH3

HC2A	TALVAEYL	TRKGV-----	-----FRQGCTAFRVITPN
KIAA	TALVAEYL	TRKEA-----	-----VQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYL	TRKEAD-----	-----LALQREPPVPFYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEFL	HRKKL-----	-----FPNGCSAFKKITPN
HC1	AALIAEYL	KRKG YWKVEKICTASLLSE	THPCDSNSLLTTPSGGSMFSGMGPFLSITPN
HC3	AALVAEYL	SMLD-----	-----RKYLPVGCVTFFQNISSN
HC5	AALVAEYL	SMLD-----	-----HSYLPVGSVSFQNISSN

ITAM

HC2A	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLI	IPI
KIAA	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLI	IPI
rat	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSP	
HC4	IDEEGAMKEDAGMMD-----	VHYSEEVLELLEQCVNGLWKAERYEII	SEISKLIGPI
HC1	IKKEGAAKEDSGMHD-----	TPYNEIILVEQLYMCGEFLWKSERYELIADVNKPI	IAV
HC3	VLEESAVSDDVVSPEEGICSGKYFTESGLVGLLEQAAASF	SMAGMYEAVNEVYKVL	IPI
HC5	VLEESVVSDDLSPDEDGVCAGQYFTESGLVGLLEQAAELF	STGGLYETVNEVYKVL	IPI

		ITAM	ITAM		ITAM	ITAM
HC2A	YEKRRD-----					
KIAA	YEKRRD	FERLAHLYDTH	HRAYS	KVTEVMHSGRRL	LGTYFR	VAFFGQAAQYQFTDSETDVE
rat	SMKSGGTLE	THLYDTH	HRPY	SKVTEVITR-----	A-----	AGSWDLLPGGLFGQ
HC4	YENRREFENLT	QVYRTIH	GAYTKILEVMHTK	KRLLG-----	-----	TFFRVAFYQG
HC1	FEKQRDFK	KLSDLYDTH	HRSYL	KVAE VVNSEKRLFG-----	-----	RYRVAFYQG
HC3	HEANRDAK	KLSTIHGKLQEA	FSKIVH	QSTGWERMFG-----	-----	TYFRVGFYQ-
HC5	LEAHREFR	KLTLTHSKLQRA	FDSIVNKDH--	KRMFG-----	-----	TYFRVGFYQ-

		ITAM		ITAM
HC2A	-FFED	EDGKEYIYKEPKLTPLSEISQRL	KLKYSDFGSENVKMIQDSGKVNPKDLDSKYA	
KIAA	GFFE	EDGKEYIYKEPKLTPLSEISQRL	KLKYSDFGSENVKMIQDSGKVNPKDLDSKYA	
rat	GFFE	EDGKEYIYKEPKLTPLSEISQRL	KLKYSDFGSENVKMIQDSGKVNPKDLDSKYA	
HC4	SFFE	EDGKEYIYKEPKLTGLSEISLRLVKLYGEK	FGTENVKIIQDSKVNPAKELDPKYA	
HC1	GFFE	EEGKEYIYKEPKLTGLSEISQRL	KLKYSDFGADNVKIIQDSNVNPKDLDPKYA	
HC3	TKFG	DLDEQEFVYKEPAITKLAEISHR	IEQFYGERFGEDVVEIKDSNPVDKCKLDPNKA	
HC5	SKFG	DLDEQEFVYKEPAITKLPEISHR	LEAFYGCFFGAEFVEVIKDSNPVDKTKLDPNKA	

4.1

ITAM

HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat	YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4	HIQVTVYKPYFDDKELTERKTEFERNHNISRFVFEAPYTLGKKQGCIEEQCKRRTILT
HC1	YIQVTVYVTPFFEEKEIEDRKTD FEMHNNINRFVFETPFTLSGKKHGGVAEQCKRRTILT
HC3	YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGEHQFQRKRTILT
HC5	YIQITYVEPYFDEYEMKDRVITYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLT

FIG. 4B (4 of 5)

	Coiled-Coil 1
HC2A	IHCFFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
KIAA	IHCFFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
rat	IHCFFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQGSV
HC4	SNSFPYVKKRIPINCEQQINLKPIDGATDEIKDKTAEQLKLCSSSTDVDMIQLQLKLQGSV
HC1	SHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV
HC3	SHAFPPYIKTRVNVTHKEEIIILTPIEVAIEDMQKKTQELAFATHQDPADPKMLQMVLOGSV
HC5	MHAFPPYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPDAKMLQMVLOGSV

	Coiled-Coil 2
HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLLDSQASKYPKKVSELKDMFRKFIQACSTALELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE
HC3	GTTVNQGGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNSLIGPVQKE
HC5	GATVNQGGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE

	Coiled-Coil 2
HC2A	YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPSTMVHGMTSS
KIAA	YQEEMKANYREMAKELSEIMHEQLG-----
rat	YQEEMKANYREIRKELSDIIVERICPGEDKRATKFPALQQRHQRDTNKHSGSRVDQFILS
HC4	YHEGLKSNFRDMVKELSDIIEHQILQEDTMHSPWMSNTLHVFCASISGTSSDRGYGSPRYA
HC1	YQEELRSHYKMDLSELSTVMNEQITGRDDLK---RGVDQTCTRVISKATPALPTVSISS
HC3	YQRELG---KLSS-----P-----
HC5	YQQELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS--

	PBM
HC2A	SSVV-----
KIAA	-----
rat	CVTLPEPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMNGGREKEPWTVIFNSRFYRSWGK
HC4	EV-----
HC1	SAEV-----
HC3	-----
HC5	-----

HC2A	----
KIAA	----
rat	VHIFF
HC4	----
HC1	----
HC3	----
HC5	----
RNTVLT	

FIG. 4B (5 of 5)

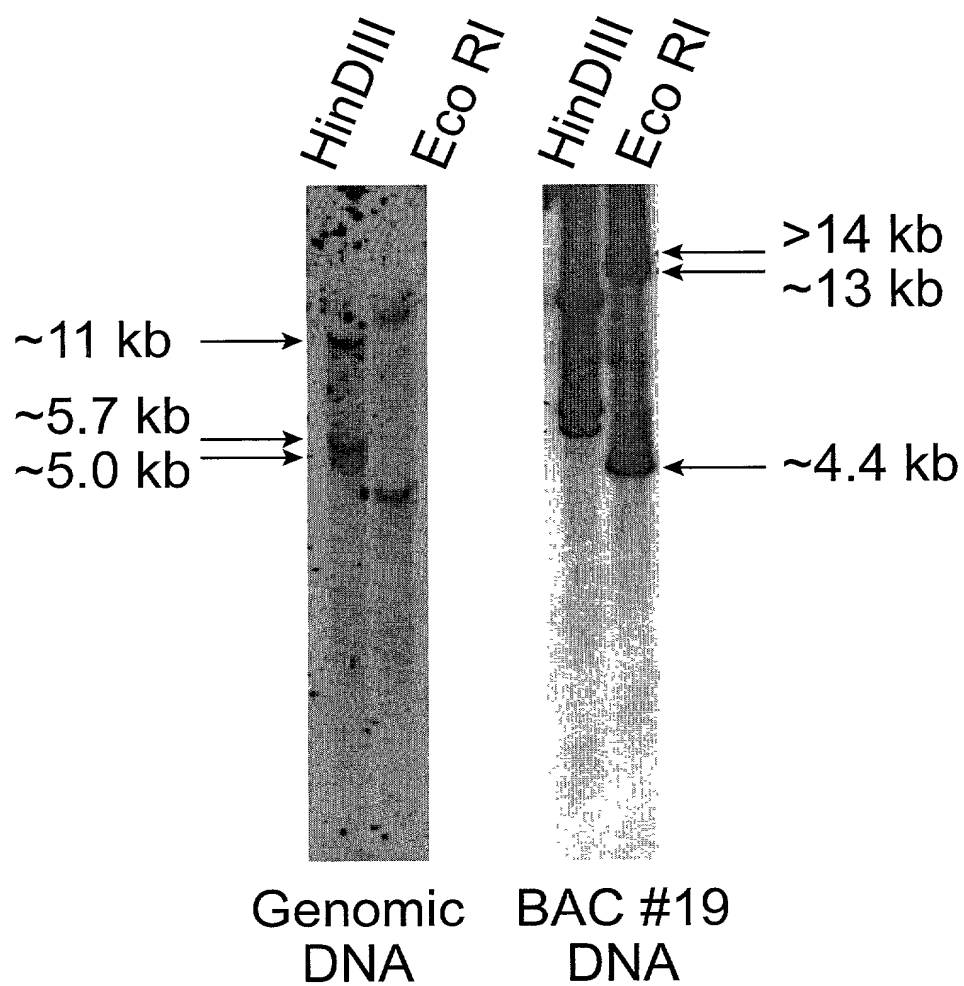


FIG. 5

-111

CGGTAACCGCCATTTTGTCTCCTGTAAACAATTTACGCGCCGTGTAAGTGTGAATCTTTCAAAGCCTCAGTTTATGACC
CTGTGGAGCCAGTGGACTTTGAAGGACTTCTG -1

1/1	31/11
ATG ACA CAC CTG AAC AGC CTG GAT GTG CAG	CTT GCC CAG GAG CTC GGG GAC TTC ACT GAT
Met thr his leu asn ser leu asp val gln	leu ala gln glu leu gly asp phe thr asp
61/21	91/31
GAC GAC TTG GAC GTG GTG TTC ACG CCA AAG	GAA TGT AGG ACT TTG CAG CCC TCT TTG CCG
asp asp leu asp val val phe thr pro lys	glu cys arg thr leu gln pro ser leu pro
121/41	151/51
GAG GAA GGG GTT GAA CTG GAC CCT CAT GTC	AGG GAC TGT GTT CAG ACC TAC ATC CGT GAG
glu glu gly val glu leu asp pro his val	arg asp cys val gln thr tyr ile arg glu
181/61	211/71
TGG CTA ATC GTG AAC CGG AAA AAC CAA GGA	AGT CCA GAA ATC TGT GGC TTT AAA AAG ACT
trp leu ile val asn arg lys asn gln gly	ser pro glu ile cys gly phe lys lys thr
241/81	271/91
GGA TCT CGA AAA GAT TTT CAC AAG ACG CTT	CCG AAA CAG ACG TTT GAG TCG GAA ACC TTG
gly ser arg lys asp phe his lys thr leu	pro lys gln thr phe glu ser glu thr leu
301/101	331/111
GAG TGC AGT GAA CCC GCT GCT CAG GCA GGC	CCC CGC CAC TTA AAC GTG CTG TGC GAC GTG
glu cys ser glu pro ala ala gln ala gly	pro arg his leu asn val leu cys asp val
361/121	391/131
TCT GGG AAA GGC CCC GTC ACT GCC TGT GAC	TTT GAC CTC CGC AGC CTG CAG CCT GAC AAG
ser gly lys gly pro val thr ala cys asp	phe asp leu arg ser leu gln pro asp lys
421/141	451/151
CGG CTA GAA AAC CTC CTG CAG CAA GTG AGT	GCC GAG GAC TTT GAG AAG CAG AAC GAG GAG
arg leu glu asn leu leu gln gln val ser	ala glu asp phe glu lys gln asn glu glu
481/161	511/171
GCC CGG AGG ACC AAC AGG CAG GCC GAG CTC	TTT GCC CTT TAC CCA TCA GTG GAC GAG GAG
ala arg arg thr asn arg gln ala glu leu	phe ala leu tyr pro ser val asp glu glu
541/181	571/191
GAT GCT GTG GAA ATA CGT CCA GTA CCA GAA	TGT CCC AAG GAA CAC CTG GGC AAC AGA ATA
asp ala val glu ile arg pro val pro glu	cys pro lys glu his leu gly asn arg ile
601/201	631/211
TTG GTC AAG TTG CTG ACC TTG AAG TTC GAG	ATT GAA ATT GAG CCC CTG TTT GCC AGC ATT
leu val lys leu leu thr leu lys phe glu	ile glu ile glu pro leu phe ala ser ile
661/221	691/231
GCC CTC TAC GAT GTT AAA GAA AGG AAA AAG	ATC TCA GAA AAT TTT CAC TGT GAC CTG AAC
ala leu tyr asp val lys glu arg lys lys	ile ser glu asn phe his cys asp leu asn
721/241	751/251
TCT GAC CAG TTC AAA GGA TTT CTG CGA GCT	CAC ACG CCT TCA GTG GCC GCA TCA AGT CAG
ser asp gln phe lys gly phe leu arg ala	his thr pro ser val ala ala ser ser gln
781/261	811/271
GCG AGA TCT GCA GTC TTC TCA GTC ACC TAC	CCG TCC TCA GAC ATC TAC CTG GTA GTC AAG
ala arg ser ala val phe ser val thr tyr	pro ser ser asp ile tyr leu val val lys
841/281	871/291
ATT GAA AAA GTC CTG CAG CAG GGA GAT ATT	GGA GAC TGT GCA GAG CCC TAC ACG GTT ATC
ile glu lys val leu gln gln gly asp ile	gly asp cys ala glu pro tyr thr val ile
901/301	931/311
AAA GAA AGT GAT GGT GGA AAG AGT AAA GAA	AAG ATT GAA AAA CTA AAA CTC CAA GCT GAA
lys glu ser asp gly gly lys ser lys glu	lys ile glu lys leu lys leu gln ala glu
961/321	991/331
TCC TTC TGC CAG CGT TTG GGG AAA TAC CGG	ATG CCC TTT GCC TGG GCA CCC ATA AGC TTA
ser phe cys gln arg leu gly lys tyr arg	met pro phe ala trp ala pro ile ser leu

FIG. 6A (1 of 6)

1021/341	TCA AGC TTC TTC AAT GTC TCC ACC CTT GAG	1051/351	AGG GAG GTA ACT GAT GTG GAC TCT GTG GTT
ser ser phe phe asn val ser thr leu glu		arg glu val thr asp val asp ser val val	
1081/361	GGG AGA AGC CCA GTG GGT GAA CGG AGG ACA	1111/371	TTG GCC CAA TCT AGA AGG CTT TCT GAA AGA
gly arg ser pro val gly glu arg arg thr		leu ala gln ser arg arg leu ser glu arg	
1141/381	GCC CTC TCC TTG GAG GAA AAT GGG GTT GGA	1171/391	TCC AAC TTC AAA ACC TCC ACT CTG AGC GTT
ala leu ser leu glu glu asn gly val gly		ser asn phe lys thr ser thr leu ser val	
1201/401	AGC AGC TTT TTC AAG CAG GAA GGA GAT CGC	1231/411	CTT AGC GAT GAA GAC TTA TTC AAG TTT TTA
ser ser phe phe lys gln glu gly asp arg		leu ser asp glu asp leu phe lys phe leu	
1261/421	GCT GAC TAC AAA AGA TCA TCA TCC TTA CAG	1291/431	AGA CGA GTC AAG TCA ATT CCA GGC TTG CTA
ala asp tyr lys arg ser ser ser leu gln		arg arg val lys ser ile pro gly leu leu	
1321/441	AGA CTG GAG ATT TCT ACA GCT CCA GAG ATC	1351/451	ATC AAT TGC TGT CTG ACT CCT GAA ATG CTG
arg leu glu ile ser thr ala pro glu ile		ile asn cys cys leu thr pro glu met leu	
1381/461	CCC GTG AAA CCC TTT CCT GAA AAC CGG ACA	1411/471	CGC CCG CAC AAA GAG ATT TTG GAA TTT CCA
pro val lys pro phe pro glu asn arg thr		arg pro his lys glu ile leu glu phe pro	
1441/481	ACA CGA GAA GTA TAT GTC CCT CAC ACT GTG	1471/491	TAC AGA AAC CTT CTC TAT GTC TAC CCA CAG
thr arg glu val tyr val pro his thr val		tyr arg asn leu leu tyr val tyr pro gln	
1501/501	AGG CTG AAC TTT GTA AAC AAA CTA GCA TCA	1531/511	GCC CGG AAC ATT ACA ATA AAG ATC CAG TTT
arg leu asn phe val asn lys leu ala ser		ala arg asn ile thr ile lys ile gln phe	
1561/521	ATG TGT GGA GAA GAT GCT AGC AAT GCG ATG	1591/531	CCG GTC ATC TTT GGA AAA TCC AGC GGG CCT
met cys gly glu asp ala ser asn ala met		pro val ile phe gly lys ser ser gly pro	
1621/541	GAA TTT CTG CAG GAA GTG TAC ACA GCT GTT	1651/551	ACA TAC CAT AAT AAG TCT CCT GAC TTT TAT
glu phe leu gln glu val tyr thr ala val		thr tyr his asn lys ser pro asp phe tyr	
1681/561	GAA GAA GTG AAA ATT AAG CTC CCC GCT AAG	1711/571	CTC ACA GTA AAT CAC CAC CTC CTG TTC ACC
glu glu val lys ile lys leu pro ala lys		leu thr val asn his his leu leu phe thr	
1741/581	TTC TAC CAT ATC AGC TGT CAG CAG AAG CAA	1771/591	GGA GCC TCC GTG GAA ACT CTC CTG GGA TAT
phe tyr his ile ser cys gln gln lys gln		gly ala ser val glu thr leu leu gly tyr	
1801/601	TCA TGG CTG CCA ATT CTC TTA AAT GAA CGT	1831/611	CTT CAA ACT GGA TCC TAC TGT CTC CCA GTT
ser trp leu pro ile leu leu asn glu arg		leu gln thr gly ser tyr cys leu pro val	
1861/621	GCC TTG GAA AAA TTG CCA CCC AAC TAC TCC	1891/631	ATG CAT TCT GCT GAG AAA GTC CCA TTA CAG
ala leu glu lys leu pro pro asn tyr ser		met his ser ala glu lys val pro leu gln	
1921/641	AAT CCT CCC ATT AAG TGG GCT GAA GGA CAT	1951/651	AAG GGA GTA TTT AAT ATT GAA GTG CAA GCT
asn pro pro ile lys trp ala glu gly his		lys gly val phe asn ile glu val gln ala	
1981/661	GTT TCT TCT GTA CAC ACC CAG GAC AAC CAC	2011/671	CTG GAG AAG TTC TTC ACC CTC TGC CAC TCC
val ser ser val his thr gln asp asn his		leu glu lys phe phe thr leu cys his ser	
2041/681	CTG GAG AGC CAG GTG ACC TTC CCC ATC CGC	2071/691	GTG CTG GAT CAG AAA ATC AGC GAG ATG GCG
leu glu ser gln val thr phe pro ile arg		val leu asp gln lys ile ser glu met ala	
2101/701	CTG GAG CAT GAG CTG AAG CTC AGC ATC ATC	2131/711	TGC CTG AAC TCC TCC CGC CTG GAG CCG CTC
leu glu his glu leu lys leu ser ile ile		cys leu asn ser ser arg leu glu pro leu	

FIG. 6A (2 of 6)

2161/721
 GTG CTC TTC CTG CAC CTG GTG CTG GAC AAG
 val leu phe leu his leu val leu asp lys
 2221/741
 ATC GCT GGC CAG ACA GCC AAC TTC TCC CAG
 ile ala gly gln thr ala asn phe ser gln phe ala phe glu ser val val ala ile ala
 2281/761
 AAC AGT CTG CAC AAC AGC AAG GAC CTG AGC
 asn ser leu his asn ser lys asp leu ser
 2341/781
 GCT TCC TAC GTG CAC TAC GTC TTC CGC CTG
 ala ser tyr val his tyr val phe arg leu
 2401/801
 GGC GCT CCC ACT GCC CTC CTA GAC CCT CGG
 gly ala pro thr ala leu leu asp pro arg
 2461/821
 GCT GCT GTG AGT TCA AAG CTG CTG CAG GCC
 ala ala val ser ser lys leu leu gln ala
 2521/841
 GCG GGG ACA CAC TCC GCA GCA GAC GAG GAA
 ala gly thr his ser ala ala asp glu glu
 2581/861
 GAT CGC AAC TGC AGC CGA ATG TCT TAC TAT
 asp arg asn cys ser arg met ser tyr tyr
 2641/881
 CCT GCA GCC CCA AGG CCA GCC AGC AAA AAG
 pro ala ala pro arg pro ala ser lys lys
 2701/901
 GTG GTC AGC ACC GGA ATG GTG AAA AGC ATG
 val val ser thr gly met val lys ser met
 2761/921
 GAC AGT TTT CGG AGG ACT CGT TTT TCT GAC
 asp ser phe arg arg thr arg phe ser asp
 2821/941
 AAT GTG GTC ACC TCG GAA ATT GCA GCC CTT
 asn val val thr ser glu ile ala ala leu
 2881/961
 GCG GAA AAG ATG AAC ATC AGC CTG GCT TTC
 ala glu lys met asn ile ser leu ala phe
 2941/981
 CGG GGC TTT GTG TTT AAC CTC ATC AGA CAT
 arg gly phe val phe asn leu ile arg his
 3001/1001
 AAC CTT CCA ACG CTC ATT TCC ATG AGG CTA
 asn leu pro thr leu ile ser met arg leu
 3061/1021
 CAT TAC CTC AAT CTG AAC CTT TTT TTT ATG
 his tyr leu asn leu asn leu phe phe met
 3121/1041
 CCT TCC ATA TCT TCC CAG AAC TCA AGC TCC
 pro ser ile ser ser gln asn ser ser ser
 3181/1061
 AGC ATG TTC GAT CTG ACT TCC GAG TAC CGC
 ser met phe asp leu thr ser glu tyr arg
 3241/1081
 ACA GAA CTG GCT GCT GCC CTG GAT GCC GAA
 thr glu leu ala ala ala leu asp ala glu
 2191/731
 CTC TTC CAG CTG TCC GTG CAG CCC ATG GTC
 leu phe gln leu ser val gln pro met val
 2251/751
 TTT GCC TTC GAG TCC GTG GTG GCC ATC GCC
 phe ala phe glu ser val val ala ile ala
 2311/771
 AAG GAC CAG CAT GGG AGG AAC TGC CTG CTG
 lys asp gln his gly arg asn cys leu leu
 2371/791
 CCA GAG GTG CAA AGG GAT GTG CCC AAG TCA
 pro glu val gln arg asp val pro lys ser
 2431/811
 AGC TAC CAC ACG TAT GGC CGC ACA TCA GCT
 ser tyr his thr tyr gly arg thr ser ala
 2491/831
 CGG GTG ATG AGC AGC AGT AAC CCA GAC CTC
 arg val met ser ser ser asn pro asp leu
 2551/851
 GTG AAG AAC ATC ATG TCT TCA AAG ATC GCC
 val lys asn ile met ser ser lys ile ala
 2611/871
 TGC TCT GGC AGT AGT GAT GCT CCA AGT TCA
 cys ser gly ser ser asp ala pro ser ser
 2671/891
 CAT TTC CAT GAG GAG CTT GCC CTT CAG ATG
 his phe his glu glu leu ala leu gln met
 2731/911
 GCC CAG CAC GTA CAT AAC ATG GAC AAA CGG
 ala gln his val his asn met asp lys arg
 2791/931
 CGT TTC ATG GAT GAC ATA ACT ACT ATT GTT
 arg phe met asp asp ile thr thr ile val
 2851/951
 TTA GTA AAA CCA CAG AAG GAA AAT GAA CAG
 leu val lys pro gln lys glu asn glu gln
 2911/971
 TTC TTG TAT GAC CTT CTC TCC CTC ATG GAT
 phe leu tyr asp leu leu ser leu met asp
 2971/991
 TAT TGC AGC CAG CTG TCA GCC AAG CTC AGT
 tyr cys ser gln leu ser ala lys leu ser
 3031/1011
 GAG TTC CTG AGA ATC CTC TGT AGC CAT GAG
 glu phe leu arg ile leu cys ser his glu
 3091/1031
 AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT
 asn ala asp thr ala pro thr ser pro cys
 3151/1051
 TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC
 cys ser ser phe gln asp gln lys ile ala
 3211/1071
 CAG CAG CAC TTC CTC ACC GGG CTC CTC TTC
 gln gln his phe leu thr gly leu leu phe
 3271/1091
 GGG GAA GGA ATC AGC AAA GTA CAA AGG AAA
 gly glu gly ile ser lys val gln arg lys

FIG. 6A (3 of 6)

3301/1101	GCT GTC AGT GCA ATT CAC AGC CTG CTA AGT	3331/1111	TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA
3361/1121	ala val ser ala ile his ser leu leu ser	3391/1131	ser his asp leu asp pro arg cys val lys
3421/1141	CCA GAG GTG AAG GTC AAA ATC GCC GCC CTT	3451/1151	TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT
3481/1161	pro glu val lys val lys ile ala ala leu	3511/1171	tyr leu pro leu val gly ile ile leu asp
3541/1181	GCT TTG CCA CAG CTC TGT GAC TTT ACA GTT	3571/1191	GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC
3601/1201	ala leu pro gln leu cys asp phe thr val	3631/1211	ala asp thr arg arg tyr arg thr ser gly
3661/1221	TCG GAT GAA GAA CAA GAA GGA GCC GGT GCC	3691/1231	ATT AAC CAG AAT GTG GCT CTG GCC ATA GCA
3721/1241	ser asp glu glu gln glu gly ala gly ala	3751/1251	ile asn gln asn val ala leu ala ile ala
3781/1261	GGG AAT AAT TTC AAT TTG AAA ACA AGT GGA	3811/1271	ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG
3841/1281	gly asn asn phe asn leu lys thr ser gly	3871/1291	ile val leu ser ser leu pro tyr lys gln
3901/1301	TAC AAC ATG CTG AAC GCG GAC ACT ACT CGC	3931/1311	AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG
3961/1321	tyr asn met leu asn ala asp thr thr arg	3991/1331	asn leu met ile cys phe leu trp ile met
4021/1341	AAA AAT GCT GAT CAG AGC CTC ATT AGG AAG	4051/1351	TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC
4081/1361	lys asn ala asp gln ser leu ile arg lys	4111/1371	trp ile ala asp leu pro ser thr gln leu
4141/1381	AAC AGG ATT TTA GAT CTA CTT TTC ATC TGT	4171/1391	GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG
4201/1401	asn arg ile leu asp leu leu phe ile cys	4231/1411	val leu cys phe glu tyr lys gly lys gln
4261/1421	AGT TCT GAC AAA GTC AGT ACC CAA GTC CTG	4291/1431	CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG
4321/1441	ser ser asp lys val ser thr gln val leu	4351/1451	gln lys ser arg asp val lys ala arg leu
4381/1461	GAA GAG GCT TTG CTG CGT GGG GAA GGG GCC	4411/1471	AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA
	glu glu ala leu leu arg gly glu gly ala		arg gly glu met met arg arg arg ala pro
	GGG AAC GAC CGA TTT CCA GGC CTA AAT GAA		AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT
	gly asn asp arg phe pro gly leu asn glu		asn leu arg trp lys lys glu gln thr his
	TGG CGG CAA GCT AAT GAG AAG CTA GAT AAA		ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG
	trp arg gln ala asn glu lys leu asp lys		thr lys ala glu leu asp gln glu ala leu
	ATC AGT GGC AAT CTG GCT ACA GAA GCA CAT		TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT
	ile ser gly asn leu ala thr glu ala his		leu ile ile leu asp met gln glu asn ile
	ATC CAG GCG AGC TCG GCT CTG GAC TGT AAA		GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG
	ile gln ala ser ser ala leu asp cys lys		asp ser leu leu gly gly val leu arg val
	CTG GTG AAT TCT CTG AAC TGT GAT CAG AGT		ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA
	leu val asn ser leu asn cys asp gln ser		thr thr tyr leu thr his cys phe ala thr
	CTC CGT GCT CTC ATC GCC AAG TTT GGA GAC		TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT
	leu arg ala leu ile ala lys phe gly asp		leu leu phe glu glu glu val glu gln cys
	TTC GAC CTA TGT CAC CAA GTC CTG CAC CAC		TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC
	phe asp leu cys his gln val leu his his		cys ser ser ser met asp val thr arg ser
	CAA GCC TGT GCC ACC CTT TAC CTC CTC ATG		AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT
	gln ala cys ala thr leu tyr leu leu met		arg phe ser phe gly ala thr ser asn phe
	GCA AGA GTA AAG ATG CAA GTA ACC ATG TCC		CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC
	ala arg val lys met gln val thr met ser		leu ala ser leu val gly arg ala pro asp

FIG. 6A (4 of 6)

4441/1481	4471/1491
TTT AAT GAA GAG CAC CTG AGA AGA TCC TTG	AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC
phe asn glu glu his leu arg arg ser leu	arg thr ile leu ala tyr ser glu glu asp
4501/1501	4531/1511
ACA GCC ATG CAG ATG ACT CCT TTT CCC ACC	CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT
thr ala met gln met thr pro phe pro thr	gln val glu glu leu leu cys asn leu asn
4561/1521	4591/1531
AGC ATC TTA TAT GAC ACA GTG AAA ATG AGG	GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG
ser ile leu tyr asp thr val lys met arg	glu phe gln glu asp pro glu met leu met
4621/1541	4651/1551
GAT CTC ATG TAC AGA ATT GCC AAG AGT TAC	CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG
asp leu met tyr arg ile ala lys ser tyr	gln ala ser pro asp leu arg leu thr trp
4681/1561	4711/1571
CTC CAG AAC ATG GCA GAG AAA CAC ACC AAG	AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC
leu gln asn met ala glu lys his thr lys	lys lys cys tyr thr glu ala ala met cys
4741/1581	4771/1591
CTG GTG CAC GCC GCT GCG TTA GTG GCT GAG	TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC
leu val his ala ala ala leu val ala glu	tyr leu ser met leu glu asp his ser tyr
4801/1601	4831/1611
CTG CCC GTG GGC AGT GTC AGC TTC CAG AAT	ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG
leu pro val gly ser val ser phe gln asn	ile ser ser asn val leu glu glu ser val
4861/1621	4891/1631
GTC TCT GAG GAC ACC CTG TCA CCT GAC GAG	GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC
val ser glu asp thr leu ser pro asp glu	asp gly val cys ala gly gln tyr phe thr
4921/1641	4951/1651
GAG AGT GGC CTG GTA GGC CTC CTG GAG CAG	GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA
glu ser gly leu val gly leu leu glu gln	ala ala glu leu phe ser thr gly gly leu
4981/1661	5011/1671
TAT GAG ACA GTT AAT GAG GTC TAC AAG CTG	GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA
tyr glu thr val asn glu val tyr lys leu	val ile pro ile leu glu ala his arg glu
5041/1681	5071/1691
TTC CGG AAG CTG ACA CTC ACT CAC AGC AAG	CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC
phe arg lys leu thr leu thr his ser lys	leu gln arg ala phe asp ser ile val asn
5101/1701	5131/1711
AAG GAT CAT AAG AGA ATG TTT GGA ACC TAC	TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT
lys asp his lys arg met phe gly thr tyr	phe arg val gly phe phe gly ser lys phe
5161/1721	5191/1731
GGG GAT TTG GAT GAA CAG GAG TTT GTC TAC	AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG
gly asp leu asp glu gln glu phe val tyr	lys glu pro ala ile thr lys leu pro glu
5221/1741	5251/1751
ATC TCA CAT AGA CTA GAG GCA TTT TAT GGT	CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG
ile ser his arg leu glu ala phe tyr gly	gln cys phe gly ala glu phe val glu val
5281/1761	5311/1771
ATT AAA GAC TCC ACT CCT GTG GAC AAA ACC	AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG
ile lys asp ser thr pro val asp lys thr	lys leu asp pro asn lys ala tyr ile gln
5341/1781	5371/1791
ATC ACT TTT GTG GAG CCC TAC TTT GAT GAG	TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT
ile thr phe val glu pro tyr phe asp glu	tyr glu met lys asp arg val thr tyr phe
5401/1801	5431/1811
GAG AAG AAT TTC AAC CTC CGG AGG TTC ATG	TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG
glu lys asn phe asn leu arg arg phe met	tyr thr thr pro phe thr leu glu gly arg
5461/1821	5491/1831
CCT CGG GGA GAG CTG CAT GAG CAG TAC AGA	AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC
pro arg gly glu leu his glu gln tyr arg	arg asn thr val leu thr thr met his ala
5521/1841	5551/1851
TTC CCC TAC ATC AAG ACC AGG ATC AGC GTC	ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG
phe pro tyr ile lys thr arg ile ser val	ile gln lys glu glu phe val leu thr pro

FIG. 6A (5 of 6)

5581/1861 5611/1871
ATT GAA GTT GCC ATT GAA GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC
ile glu val ala ile glu asp met lys lys lys thr leu gln leu ala val ala ile asn
5641/1881 5671/1891
CAG GAG CCG CCT GAT GCA AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT
gln glu pro pro asp ala lys met leu gln met val leu gln gly ser val gly ala thr
5701/1901 5731/1911
GTA AAT CAG GGA CCA CTG GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA
val asn gln gly pro leu glu val ala gln val phe leu ala glu ile pro ala asp pro
5761/1921 5791/1931
AAA CTC TAT CGA CAT CAC AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT
lys leu tyr arg his his asn lys leu arg leu cys phe lys glu phe ile met arg cys
5821/1941 5851/1951
GGT GAA GCT GTA GAG AAA AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG
gly glu ala val glu lys asn lys arg leu ile thr ala asp gln arg glu tyr gln gln
5881/1961 5911/1971
GAA CTC AAA AAG AAC TAT AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA
glu leu lys lys asn tyr asn lys leu lys glu asn leu arg pro met ile glu arg lys
5941/1981 5971/1991
ATT CCA GAA CTG TAC AAG CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC
ile pro glu leu tyr lys pro ile phe arg val glu ser gln lys arg asp ser phe his
6001/2001 6031/2011
AGA TCT AGT TTC AGG AAA TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA
arg ser ser phe arg lys cys glu thr gln leu ser gln gly ser OCH

GAAAAGCCATCTTCATTCGTGGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAATGGGACATT
TGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTCTGGAAGCTTTGGGATCCCAGGAACCATGGAATTATT
CCCAAATGGACTCTGACCAGATTTTTGCCATACTGGGGGTGGCGGGATGGAGGATGGGTACTCAGGCATGACTGCGTAT
TTATTAAAGTGTGTTTTTCCACAATGTACCAACAAGGCATAAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATC
TGAGAGATGATTTCTCTGCCCCATATTTGAATTTATGGAGTAACCTCAAATTCCTGAGGAAAAATGGAAAAATTATCC
ACCAGTCGATTCAAACTGAATTTCACTCTTTATAGGAAGGCAGGGCAAACCTGTAGGAGTACGAAACATTTTCAATAAAT
CTACAAAGGGAAGCCTTACTACAATTCAAAAATCATCATGGTTGGAAATTTGGGAGGAGATTATTTGTGAACCTGTTAC
CCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTATTTTTGTTTTATTATTACTGTTACATTAATTTAACATGCATTTA
TAGAAGAATACATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAAATCACAGATACTGCTTT
CACTTAAATGGAAACAATTCTCCGATAATGCTTTGCTTTTTTCTTATGTCACTCTGTGTACTATCTATTTTTCTCCTC
TCTGGGACCAAGTTTCTTTTATAAAGCAATAATATCTCTGTTTTCATTTTCAAGACATTGTGCTGTCTGTCAGCATATGT
ATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTGACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTG
AGAATTAATTTATATATTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAATTGCAAGCTAAAAAA
AAAAAAAAAAAACTCG

FIG. 6A (6 of 6)

A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-5 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1727	C to T change; mis-sense mutation changing codon from alanine to valine
2	1749	A to G change; silent mutation
3	2277	G to C change; silent mutation
4	2853	C to T change; silent mutation
5	3427	A to G change; mis-sense mutation changing codon from lysine to glutamic acid
6	3777	C to T change; silent mutation

B. Alternative splices

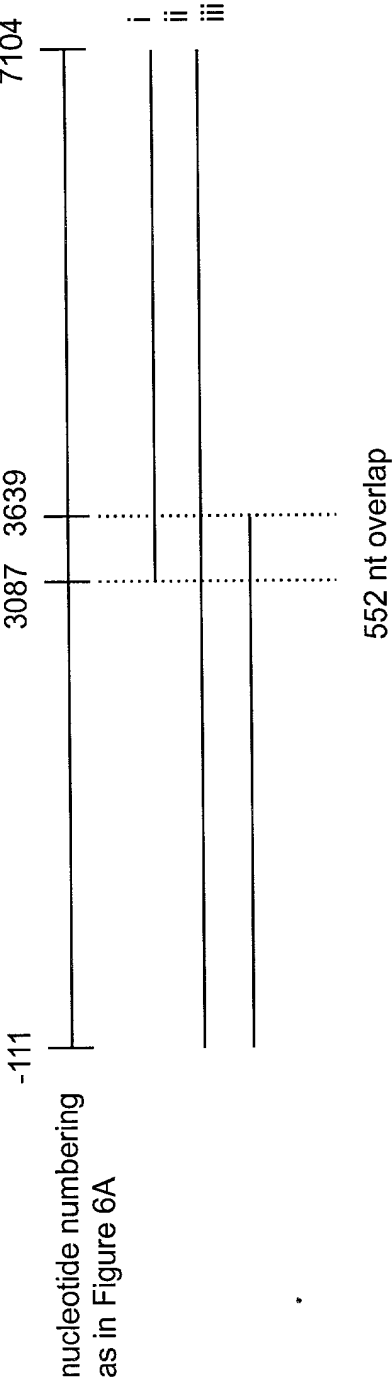
Isoform	Difference	Nucleotide(s)	Consequence
1	exon deletion	1806-1944	premature, in-frame stop codon leading to the production of a truncated, most likely soluble protein
2	exon insertion	between 2857 and 2858	additional, in-frame 48 nucleotide exon that contains a stop codon at the second codon, which would lead to a truncated, most likely soluble protein

These differences may be found separately or together in various combinations in the different human CLASP-5 isoforms

FIG. 6B

FIG. 6C

C



1st partial exon (nucleotides 3793 to 3952)

CCAGCTGTCAGCCAAGCTCAGTAACCTTCCAACGCTCATTTCCATGAGGCTAG
AGTTCCTGAGAATCCTCTGTAGCCATGAGCATTACCTCAATCTGAACCTTTTT
TTTATGAATGCTGATACTGCTCCAACATCTCCTTGTCTTCCATATCTTCCCAG
GTAATAAAAGAATTATTTAACTAAAAGAATTATTCAAGCTAT

2nd exon (nucleotides 5809 to 5948)

GCTCATAAAATGGCTCCTTACGTTTCTGTAGAACTCAAGCTCCTGCTCCAGCT
TCCAGGACCAGAAGATCGCCAGCATGTTTCGATCTGACTTCCGAGTACCGCCA
GCAGCACTTCCTCACCGGGCTCCTCTTCACAGAACTGGCTGCTGCCCTGGATG
CCGAAGGGGAAGGGTATGTTTCTGGCATTATAAAATGGAAGATGAAGC

3rd exon (nucleotides 13662 to 13831)

CATAACCTCTTGATTCCCTGTGTTGTGCCAACAGAATCAGCAAAGTACAAAGG
AAAGCTGTCAGTGCAATTCACAGCCTGCTAAGTTCTCACGACCTGGACCCAC
GCTGTGTCAAACCAGAGGTGAAGGTCAAAATCGCCGCCCTTTACCTACCTTTA
GTTGGCATCATTTTGGATGCTTTGCCACAGCTCTGTGACTTTACAGGTAATGG
CCCTTCTGTTTTCTTTCTTGGATTG

4th exon (nucleotides 16948 to 17087)

TGTTTGACTTGACATCACAAACGATGTTTTTCATTGCAGTTGCAGATACTCGCA
GATACCGCACCAAGTGGCTCGGATGAAGAACAAGAAGGAGCCGGTGCCATTA
ACCAGAATGTGGCTCTGGCCATAGCAGGGAATAATTTCAATTTGAAAACAAG
TGGAATAGTGCTGTCTTCCTTGGTATGTTGGTGCACATGTGTCTGGTTGATTTT
TCAT

5th exon (nucleotides 19281 to 19463)

TGGCCTCCATCCCCCAATCTGCCTCCCTTCAGCCCTATAAGCAGTACAACATG
CTGAACGCGGACACTACTCGCAACCTCATGATCTGCTTCCTCTGGATCATGAA
AAATGCTGATCAGAGCCTCATTAGGAAGTGGATTGCTGACCTGCCATCAACG
CAGCTCAACAGGATTTTAGATCTACTTTTCATCTGTGTGTTATGTTTTGAGTAT
AAGGTAAGTCTGGAGTGGCACAACTTTATAACCAGC

6th exon (nucleotides 19829 to 19958)

CACCAAAGGACATGTCCTCCTACCTCTGTCTTGTCCAGGGAAAACAGAGTTCT
GACAAAGTCAGTACCCAAGTCCTGCAGAAGTCAAGGGATGTCAAGGCCCCGG
CTGGAAGAGGCTTTGCTGCGTGGGGAAGGGGCCAGAGGGGAGATGATGCGC
CGCCGGGCTCCAGGTGTGTTGGACTGGCCCTTCCTGCTCTCTGTCAAGC

FIG. 7A (1 of 4)

7th exon (nucleotides 20928 to 21015)
TCAAATTCCTATCATGCATTTCTTAACTCCTAGGGAACGACCGATTTCCAGGC
CTAAATGAAAATTTGAGATGGAAGAAAGAGCAGACACATTGGCGGCAAGCT
AATGAGAAGCTAGATAAGTGAGTCACTCGGCAACTTTCTGCTACTTTTACCT

8th exon (nucleotides 25765 to 25861)
GCTTTAATTTGACCTCTTGTTGTTTCCTAGAACAAAGGCCGAGTTAGATCAAG
AAGCCTTGATCAGTGGCAATCTGGCTACAGAAGCACATTTAATCATCCTGGA
TATGCAGGAAAACATTATCCAGGTGAGGAAAACAAACACCCAATCTGATTTG

9th exon (nucleotides 27242 to 27376)
GGATTCAATGATGCTGTTCTTCCATTCCCCAGGCGAGCTCGGCTCTGGACTG
TAAAGACAGCCTGCTGGGAGGTGTTCTGAGGGTGCTGGTGAATTCTCTGAAC
TGTGATCAGAGTACCACCTACCTGACTCACTGCTTTGCAACACTCCGTGCTCT
CATCGCCAAGGTAAACTTGGGATGCTTGTTTTCTTCCTCTTAATT

10th exon (nucleotides 28582 to 28734)
AGTGATGCCTAATGGCCCTTTATGTCTCTCCTAGTTTGGGAGACTTACTCTTCG
AAGAGGAGGTGGAACAGTGTTTCGACCTATGTCACCAAGTCCTGCACCACTG
CAGCAGCAGCATGGATGTCACCCGGAGCCAAGCCTGTGCCACCCTTTACCTC
CTCATGAGGTTCAAGTTTTGGAGCCACCAGTGTAAGAGTTCAAACCAGCTGAG
TGACCTGGAATCAG

11th exon (nucleotides 31046 to 31204)
TTACTTCATCTTTTTTTTTTTTTTTCCTGATGCAGAAATTTTGCAAGAGTAAAGA
TGCAAGTAACCATGTCCTTGGCATCTTTGGTGGGAAGAGCACCAGACTTTAA
TGAAGAGCACCTGAGAAGATCCTTGAGGACAATTTTGGCCTATTCAGAAGAG
GACACAGCCATGCAGATGACTCCTTTTCCCACCCAGGTACACCGAAGCACAT
ACCTTGCTCATGCATGAGT

12th exon (nucleotides 32755 to 32855)
AGCTAAGATTATTTTGGAGGCTTACACTTTTTTGCAGGTGGAGGAACTTCTCTGT
AATCTGAATAGCATCTTATATGACACAGTGAAAATGAGGGAATTTTCAGGAAG
ATCCTGAGATGCTTATGGATCTCATGTACAGGTAAGCTTTCCTGACACACTCA
AGGGACACCATT

13th exon (nucleotides 33663 to 33855)
TCCTCAAACTACTTCTCACTCAATCTGTCTTCAGAAATTGCCAAGAGTTACCA
GGCATCTCCTGATCTGCGGCTGACCTGGCTCCAGAACATGGCAGAGAAACACAC
CAAGAAGAAGTGCTACACGGAGGCTGCCATGTGCCTGGTGCACGCCGCTG
CGTTAGTGGCTGAGTATCTGAGCATGCTGGAGGACCACAGCTACCTGCCCGT
GGGCAGTGTGAGCTTCCAGGTAGGGTGTGTGCAGCTTTTCCCTTAGAGCAGTG
GTTC

FIG. 7A (2 of 4)

14th exon (nucleotides 38125 to 38268)
CTGTTCTCCAGGCTTATACTGTGGTCTCTTTTCAGAAATATTTCTTCCAATGTGCT
GGAGGAGTCTGTGGTCTCTGAGGACACCCTGTCACCTGACGAGGATGGGGTGTG
CGCAGGCCAGTACTTCACCGAGAGTGGCCTGGTAGGCCTCCTGGAGCAGG
CCGCGGAGCTCTTCAGCACGGTCAGTGCCCAGAGGGCATCCCGGGGCCTGGC
C

15th exon (nucleotides 40166 to 40297)
AATTCTCTCTGATGCTCTTCTCCTCTTTTCCAAGGGAGGCTTATATGAGACAGT
TAATGAGGTCTACAAGCTGGTCATCCCCATCCTAGAAGCGCATCGAGAATTC
CGGAAGCTGACACTCACTCACAGCAAGCTGCAGAGAGCCTTCGACAGCATCG
TTAACAAGGTAGCCGGGGAGCCTGGCTGGCAGGTCTTGTTAC

16th exon (nucleotides 40755 to 40889)
TAAGGAGAGCTTTTTTATATTTTGGTTCCTCAGGATCATAAGAGAATGTTTGGAA
CCTACTTCCGAGTTGGTTTCTTTGGATCCAAATTTGGGGATTTGGATGAACAG
GAGTTTGTCTACAAAGAGCCTGCAATTACCAAGCTTCCTGAGATCTCACATAG
ACTAGAGGTAAGAAAAGTGATTCTGTGCGCCTGACCTGGTACACTTTAC

17th exon (nucleotides 42307 to 42396)
AACCTTTATAAACTGTTGGTTCTTCTTACCTAGGCATTTTATGGTCAATGTTTT
GGTGCAGAAATTTGTGGAAGTGATTAAAGACTCCACTCCTGTGGACAAAACCA
AGTTGGATCCTAACAAAGGTATACAAAAATTTACAAAACTAACCATCAAGC

18th exon (nucleotides 45250 to 45486)
TCTTCTCCCTCCGTGCCTTTTCCCCCTTAGGCCTACATACAGATCACTTTTGTG
GAGCCCTACTTTGATGAGTATGAGATGAAAGACAGGGTCACATACTTTGAGAAGA
ATTTCAACCTCCGGAGGTTTATGTACACCACCCCGTTACCCCTGGAGGG
GCGGCCTCGGGGAGAGCTGCATGAGCAGTACAGAAGGAACACAGTCCTGAC
CACTATGCACGCCTTCCCCCTACATCAAGACCAGGATCAGCGTCATCCAGAAG
GAGGAGGTAATGCACCCAAGGGATTGGCCACCACTGGATGAGT

19th exon (nucleotides 48664 to 48807)
ACAGTGA CTTCCTATGTTTACGTCTCATGTT CAGTTTGT TTTGACACCGATTG
AAGTTGCCATTGAAGACATGAAGAAGAAGACCCTGCAGTTAGCAGTTGCCAT
TAACCAGGAGCCGCCTGATGCAAAGATGCTTCAGATGGTGCTGCAAGGCTCTGT
GGGAGCTACTGTAAATCAGGTAAGCAAAACCAGAGGTGGCAGCTCCT

20th exon (nucleotides 50892 to 50998)
TATATTCTTTTTTTTTTTTTTTTTTTTTTTTCCACCAGGGACCACTGGAAGTAGC
CCAAGTGTTTTTGGCTGAAATTCCTGCTGATCCAAACTCTATCGACATCACAACA
AGTTGAGGTTATGCTTTAAGGAATTCATCATGAGGTAAGAAGGAAAATG
GCTGGGAATTT CAGTAGAG

FIG. 7A (3 of 4)

21st exon (nucleotides 62398 to 62568)
TCATTTATTTCTCCACACTGATATTTTCATCTCAGATGTGGTGAAGCTGTAG
AGAAAAACAAGCGTCTCATCACGGCAGACCAGAGGGAATATCAGCAGGAAC
TCAAAAAGAAGCTATAACAAGCTAAAAGAGAACCTCAGGCCAATGATCGAGC
GGAAAATTCCAGAACTGTACAAGCCAATATTCAGAGTTGAGAGTCAAAAGAG
GTAAGAACAGGGCAGAGGAGGCCTCTTCCTGTGGGAT

22nd exon (nucleotides 63040 to 63294)
CCTCCCTCTCTTTTCTTAATTTTCAGGGACTCCTTCCACAGATCTAGTTTCAGGA
AATGTGAAACCCAGTTGTTCACAGGGCAGCTAAGAAAAGCCATCTTCATTCGT
GGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAAAT
GGGACATTTGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTC
TGGAAGCTTTGGGATCCCAGGAACCATGGAATTATTCCCAAATGGACTCTGA
CCAGATTTTTGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGC
ATGACTGCGTATTTATTAAAGTGTGTTTTTCCACAATGTACCAAACAAGGCAT
AAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATCTGAGAGATGATTC
CTCTGGCCCATATTTGAATTTATTGGAGTAACTCAAATTGCCTGAGGAAAAAT
GGAAAAATTATCCACCAGTCGATTCAAACCTGAATTTCACTCTTTATAGGAAG
GCAGGGCAAACCTTGTAGGAGTACGAAACATTTTCAATAAATCTACAAAGGGA
AGCCTTACTACAATTCCAAAAATCATCATGGTTGGAAATTTGGGAGGAGATT
ATTTGTGAACTTGTTACCCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTAT
TTTTGTTTTTATTATTACTGTTACATTAATTTAACATGCATTTATAGAAGAATAC
ATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAA
ATCACAGATACTGCTTTCACTTAAATGGAAACAATTCTCCGATAATGCTTTGC
TTTTTTTCTTATGTCACTCTTGTGTACTATCTATTTTTCTCCTCTCTGGGACCA
GTTTCTTTTTTATAAAGCAATAATATCTCTGTTTTTCATTTCAGAACATTGTGCTG
TCTGTCAGCATATGTATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTG
ACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTGAGAATTAAATT
ATATATTTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAA
TTGCAAGCTAAAAA

FIG. 7A (4 of 4)

CATTATCCTCTCTCAGTTACAGGCCCCCTCAAGTAACCACTATTCTGACTCTTATTATTAGAAATTAATACTGCCTGTT
 GTTGAATTTTCATAGTCTTTTGTGAATGTTGTGACTGTGACATCCTTTAGTGTGGTGCATGTGTGAGTATTCATTTTTT
 TTCAACTGTATGTCATATTCCTTTGTCTACTATAATTTCTCTTCTGTAAATTGACATTTGGGCTGCTTTCTATTTGTGGG
 TATTGGGTATTATGAAAACAGCTGCCGTGAACATGCCTGTGCATGGTTTTGGGTGGACGTTAGAACTCATTTCTTTGGGG
 CTATAAATACAGCCTATTTTTTATTTAATATACTGCTCTTGAATAGTTTAATAAATATGTGTACATGGTCTTAACAAA
 TGTCAAAAGAATATACTCTGAGCTAGGAAAAGAAGAGCAAAAGTCAAAGCAGGAAGATGGCAGGGAATAACAAAGGTG
 ATAGCCAAAATAAATGAAATAAAGAATAGAAAACAATCACGGAAATCCGCAAGATGAAAAGCTTGTATTGTGAAAAGAG
 CAACAAAATTCACCAATCTTTAGCTGAGCTGACCAAGAAAAAGGAAGAAGACTCAATTACTAAAAATCATAATTGAAAGA
 TTCAACACAATCATATCACAAGAGACCTTACAGAAATAAAAAGGATTATAAAGAATACGATGAACAATTGAAAGCCATC
 AAATTGATAACCTAGATTAAATGGATAAATTCCTTAAAAGGTACAAAGTACTAAAATTGACTCCAAGAAGATATAGAAA
 TCCAAATAGACCTACAGAAGTAAAAAGATTGAGTTAGTAATCAAACCTCCACATACACCTACTATGTACCCACACAAAT
 TAAAAATTTAGGCTGGGCGCAGTGGCTCATACCTGTAATCCCAGCACTTTGGGTGGCCAAGGCGAGTGGATCACCTGAGG
 TCAAGAGTTTCAAGCAGCCTGGCCAAGGTGATGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGTGTGGTGG
 CGGGAACCTGTAATCCCATCTACTCGGGAGGCTGAGGCAGAAGAATCATTGAGACTGGAAGGCAGAGGTTGCAGTGAGC
 CAAGATCATGCCAATGCACTCCAGCCTGGGCAACAAGAGCAAACTCCATCACAATAATAATAATAATAATATATT
 TTAATAATTTAAACTTCCTACAATAAAAGCTCAAACCTGGGGGGCTTTACTGATGAATTCTACCAATATTTTTAAAGA
 ATTAATTTCTAATTTTTTACCAACTTCCAGTCTTCTCTTCCAACGATGGAAGAGGTGGAATACTTCCCCACTTGTCTAT
 GAAGCTAGCATTACCTATACTAAACCAGACAAAGACATCATGAGAAAACCTACAGGCCAGTATCTGATGAATATAGATGT
 AAGACCTCAACAAACACTAGCAAACCTGAATCCAACAGCATATAAAAAGGATTATACACCATGGCTAAGTAGGATTTATC
 TCAGGAATGCAAGATAGGCTGCATACCTGAAAATCAATTGTTGTACCATATTAATAAAATAAAGGACAAAACCCATACAA
 TCATCTTAGTAGATGCAAGAAAAGCATTTAATAAAATCTAATAACGCTTCTTGATAAAAAACACTCAACAAACCTTTTAG
 GAAATAAGAGAACTTCCTCAACTTGACTTAAGGGCCTCTATGAAAAATCCACAGCTAATGTGACACTTATTAGTGAAAA
 CAGTGCTTTATCCCTAAGATTAGGAACAAGACAAAAATGTCTACCTTGGCACTTCTATTCAACATATAGGAGTTCTAT
 CTAGGGCAATTAGGCCAAAAAATAAAACAAAAGACATCTAGGCCAGGCGTGGTGGCTCACGCCCTGTAATCCCAGCACTTT
 GGGAGGCCAAAGTGGACAGATCGCTTTGAGCCCAGGAGACTGAGAACACCCTGAGCAACATGGCAAAACGCCATCTCTAC
 AAGAAATACAAAAATTAGCTGGGCATTGGTGGCTTGTGTTTGTAGTCCCAGCTACTTGGGAGGTTGAGGCTGGGAAATTG
 CTTGATCCCAGAAAGCGGAGGTTGTAGTGAGCTGAGATCACGCTACTGCACTCCAGCCTGGGCCACAGAGTAAGACCTG
 TCTCAAAAAAAAAAAAAAAAAAGAAAAAGAAAAAGAAAAAGAAAGCATTAAATTGGAAGAAGTAAACTATCTCTAT
 TCATAGGTGGCATAATCTTGTTTATAGAAAACCATAAGGAATCCACAAAAAACCCTCATTACAACCTAATAATGAATTCAG
 CAGTGTTCGATGGTATAAGATCAACATACAGAATCAATTGTGTTTCTATACACTTACGATGAGCAATCTGAAAATGAAA
 TTAAGAAAACAATTTATATAAAATAGCATCACAAAGAAAAAATATTTAGGAATAAATGTAAACAAAGAAACACAAGAGT
 TATACACTAAAAATGACAAAACACTGTTGAAAGAAAGATATAAATAAATGGAGGATATCATATGTTTCATGAATCAGAAGA
 CTTATTATTAATAATAGCAATACTCCCCAAATTGATCCATAGATTAAATGCAGTTCCTTCTCAGAATTCTAGCTTGCTTTTT
 TTTTTTTTTGGCAGAAATTAGCAAACCTGATCCTAAAAATCGTGTGGAAATTCAGGGACCCAGTATAGCCAAAACACCT
 TGAAAAACAAGAACAATAATGGAGGACTCACACTTCCCAATTTCAAACCTTACTACAAAGCAAAAGTAGTCAAGACTATG
 GGGTTCTGCATATGATAGACATATAGATCAATGAAATTGGGTTAAGAGTCCAAAAATAAATCTTCATATTTATAGTCAA
 TTGATTTTTTGACAAGAGTGCCAAAACAATTCAATGGGGGAAAAATAGAATTTTCAATAAATGGTGTGGGACAACCTGGGTA
 TCCACACTCAAAAGAATGAAGTTGGACCCCTATATTACACTGTATACAAAACTAACTCAAAATAGATCAAGACCTAAATG
 TAAGAGCTAAAACTATAAAATTGTTACATAAAATTATAGAGGTAATCATCATAGACTTAGAAAAGGCAGTGGTTTCTTAG
 ATATGACACACTCGAAAGTATGAGTAACAAGAAAAAATAGATAACTGGACTTCAGTAAATTAACACTTTTGTGATTTA
 TAGGACACCATCAAAAAAATGAAAAGGCAACACACAAAAATGGGAGAAAAATTTGCAAAATCAAAAACCTAATAGGGGACT
 TGTATCTGGAATATATATTTTAAATCTTACAACCTCAGTAATAAAAAGACAAATAACTCAGTTTTTTAAAGGCAAAAGA
 TCAGAATAGACATTTCTCCAAAGAAGATACAGCCATAAGACCATGAAGATGTTGAGCATCATAGCCGTCAGGGAGATGC
 ATATTAAAAATCACAATTAATAACCACTTGATACCCACGAAGATGGATATAATAAAAAAGACAGGTAATAAAGTGTGGCA
 AGAATAAAATGGAGTCTTCAGACACTGCTGGTGGGAATGTAAATTTGTGCAGCCACCGTTGAAAACAACCTTGCTGATTCC
 TCTAAAAGTTAAACAGAGGCTGGGCGCTCGGCGGCTCACGCCCTATAATCTCAGCACTTTGGGAGGCTGAGGTGGGCAGAT
 CATTTTGAGGCCAGGAGTTTCGAGACCAGCCTGGCCAAGATGGTGAACCCCTGTCTCTACTAAAAATACAAAAATTAGCCAG
 GTGTGGTGGCAGGTGCCTGTAGTCCCCGCTACTTGGGAGGCTGAGTCAGAAGAATTGCTTGAACCCAGGAGGTGGAGGTT
 GCAGTGAGCCGAGATCGTGTCTATTGCACTCCAGCCTGAACCACTCCATGTCAAAAAAAAAAAAAAGTTAAACAGACAGTT
 ACCATACAAGCCAGCAAAATGTAATCTGAGGTATGTACCCAAGAAAAGTAAACCTTAAACCTTGATACACATACTCATAG
 CAGCGTTGGTAAGTCACAATAGCTCAAAAGCAGAAACAATCCAATGTTTATCAGTTGATGAATGGATAAAATTCACCAA
 TGGAATATTATTTAGCAATAAAAGGAATGAAGTACTGATGCTACAATATGATAAACTTAAAAACATCATGCTAAACAGC
 AGACCCAGGTTAGAACACAGGCAGTCTGTTTCTGGATTCTATGTAGTTCTATCCTATATTGCTTGGTTTTCCAGGGTTA
 GAACACAGGCAGTCTGTTTCTGGATTCTATATAGTTCTATCCTGTATTGCTTGGTTTTCCAGGTTAGAACACAGGCAGT
 CTGTTTCTGGATTCTATGTAGTTCTATCCTGTATTGCTTGGTTTTCCAGGGTTAGAACACAGGCAGTCTGTTTCTGGATT
 CTATGTAGTTCTATCCTATATTGCTTGGTTTTCACAGTCACCTCATTGCTTAGGAGCGTTTTTCATCACTCTTGACTGTTT
 AAGAGCTCTTTAGTCAATTTCTTTTACCATAACCTCTTGATTCTGTGTTGTGCCAACAGAATCAGCAAAGTACAAAGG

FIG. 7B (3 of 15)

AAAGCTGTGCAGTGC AATTCA CAGCCTGCTAAGTTCTCAGACCTGGACCCACGCTGTGTCAAACCAGAGGTGAAGGTCAA
AATCGCGCGCCTTTACCTACCTTTAGTTGGCATCATTTTGGATGCTTTGCCACAGCTCTGTGACTTTACAGGTAATGGCC
CTTCTGTTTTCTTTCTTGGATTGTTGGGGGCCCTGCCAAATGCCCATCCGAATGAGATCTCTGTCATTTCGTTCAGTG
CTGATATGTTTCATATGAGCAATCTTCACAAAAATGGTCTCCAAACCTCTTTAACACTGGCCCCCAATCAGTTAAAAAAAC
AAAAAAAGTCACATAGCCCCATGTGTTTTTTGGTTAGAAATATTTTACTGTTTCTTCATTCATCTTTATTCATCT
ATTGATCTGCTAGTATGGAATGAACTTATATAAACCATACACCAAAGAGTGAATAATAACAAGATTACTGCCTTTGGA
GATCGTGCTTAACACCTTGAAATAAAGGTTCTCCTTCCCTTTTCTTTTATGAATATGTAAGCAAAAAAGCGGTCTCAA
GAAACCCAATAATTGCTCCATGCAAAAAAAATCATGGCATATGTCAATATTAGAAAATTCTATCATAGCAGAGAAAT
ATTGCCCTTGGCCTAAGTGACTAATTTTGGAGTTAATATGTCATAGATTAGCAACAAGATGAAAGGATAAGTTGTCTTAA
AGGGGTTTTGTGAAACCCAGAAATCTATTTACAAATTACATTGTGGATTAAAGGAATGTAGAGGGAAAAATCTCCCAA
ATAGAAGAATCTTCTATGTTGACCTGAGAAAGGCAGTCCATTGGCTACCTCTCCACAGCTACGTTGTGTGACAGTG
TGTGCGCGCTGCACACACACACACACAATCTTATCCCATCAGAGTAGTTCTTGCTTTTCTCCAGCTCAAGGGAAG
TTTTGGAAATGTCATGCTGCTCTCTTGGCAGCTGAAGGTTGCTGGGATCTGGGCAATGCTTCCCTGAGCCAGCTCTTT
ATAGTCAGTCATCCTTGAATCTTGAACCATCCAGGTTTTTCCACCTCTCCAAATGGAAGTGTATGTGTGACTAAA
TTGTTTATAATACTATTACGGTGACAAGTATTTAGTTTCATGAAAAATGGGACCAACGCCCTATAGTCTTTAATTCATACA
ATCATAAAATGAAAAGCAAGTATTCCTGTGGAAGTAATCTCTCTCTTTCTTGAAAAAAATCTCTAGCAACTGCTAATG
GAGTAACTCAGAAGAGAAAGGTTGAGACAGGGGTTAGGTTTGTAGAGTTCTGTTGGGGCAGAGTGCAAGGAAATGATA
GAAACAGCTCAGCAGACAGGGCTGAGCAAGCTGCACCATGAGTTCAGTTCAGCTTCTCTTAGCAGCGCTGATTGCGCGGA
ATTTGAAATGGAGTTGTTTTTAAACATTACAGACATAATGCAGAGCATGGCATGTGACTTGTAGCCCATTTTGAGAAATCC
TTGATGGCAAGTTTCTAAAAAGTTCCATTTCAGAGCTTGCTTGTCCCAAAGCCAGGAACCACTTTAGCACACATTATC
CGAAGTTTTCTTGTCAATTAGAATATTCGGTATCAGTGACTCGGAATCAGAATCTTTTCAACATTTGGTCTCCAAGCTTT
TAAACCTCAAAGACTTCTTTGTATATCGCTTGAACCTTTATGATCATGATGTAGCTGATGAGAGAAAAAACAGTGAAAAG
TATTTTATTTGTTATAGTTTACACAGTACATCTATTAAATAGGAATCTTTAGGTTGATAAATCATAAGAATACAGTCTT
TCAAAAAGATGCATCTGAAATCAGATTTCAGCCCCATTTTATTAATATAAGTGACCTTTGAAAGGCTCAACCTTTCCGTGC
CTTCTCTTCTCTGTAAACTATAAAAAATGTGATAACGATGTCTACCTTTTAGGTTTACGATAAAGGTGAACTAGAGAAC
TTCTATAAAAGCATTTTGCACAGCACATGTTTGTATCTTTCCCGATTTTTCTTGTAACATAAACCTATGGCAATTAAGG
GGAAATAAGAATGTGTCTCTATGTTAGTTGTGATAATGTTACAGGTCTTGCATAATTTCCATGTGCTGTTTATTTAAC
ATTTGTTTAAAAATCCCAATGGCCTTAATAAGTATTTCTAAAAATTTGGGTTTTGGCTCGGTTGGTGGCTCACCCTGTAA
TCCCAGCATCTTTGGGAGGCCAAGGTGGACAGATCTTTGAGGCCAGGGGTTCAAGACCAGCCTGGCCAACATGGCGAAAC
CCTGTCTCCCATGAAAAATACAAAAGTTAGCCAGGCGTGGTGGCGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGTAG
GAGGATGGAGGGGCAGAGATTGCAGTGAGCGGAGATGGCGCCACTGCACCTCCAGCCTGGATGATAGTGTGAGACTTTTGT
TAAAAATAAATAAATAAATAAATAAAGAACTGGGTTTTGTTTTTCAACAATTTAGTAGAAGAAATGTTATTTTACACTCA
AATTTTTCTAAATAATTGAAGGCCAGATGGCTGTAATGTCACAGGCTAGAAAAACATGAATTTTGGAAAAACATGA
GTGAATCAATCAGTTGTGAATGTTTTTACCACACTTTTCCGAACTGCTTGAATATTAATAGTCTTTTGTATGTATACTG
GTAGCATCTTTTAAAAACAGACTTTTAAACGGTTTATCGTTTTTTTTGCTTGCATACATCTAGACCTATCTATAAATATGG
GTATGTCTATATTACATAGATACAATAAATTGACATTCATTTTAAACATTTGAAATATGACAATATTGCTGAACTTGT
GATAATAGCTTATTATCTATATAAGGTAGTTGCTTAATCTGTAATTGTAGGTGTCTTCTATTTGGTCAATTATTTAAAA
TAATGCCAATTATTAGAATAGAGAATGAAGTTTAAAAAATTTATGTTACAGGAACAATATTGGAAGGTTTAAAACTTTT
TGTTACACAAATTTGAAAAATTAATTTCTAGCCTAATCTTGTGCTAGACATTTGCTTATAGCTGCTGTGTTTTCTTATA
GGTGATAGCAGATACATAATGCTFAAACATCAGGTTTGAATATTACTGTGCTGACTTTAGTGACTGAGAAGTATCAGTCTCT
TATTGGGTAGGGGACATGGGGAATGTCATGTTGACTTGACATCACAACGATGTTTTTATTGCAAGTTGCAGATACTCG
CAGATACCGCACCACTGGCTCGGATGAAGAACAGAAGGAGCCGGTGCCATTAAACCAGAATGTGGCTCTGGCCATAGCAG
GGAATAATTTCAATTTGAAAACAGTGGAATAGTGCTGTCTTCTTGGTATGTTGGTGCACATGTGTCTGGTTGATTTTT
CATTTTCATGTCTTCTGTCTTCTGTTTTGTTTTGTTTTGTTTTGTTTTGAGACAGAGCTCAGCTGTTGTCAGAGGCTG
GAGTGAGTGGCGCAATCTCAGTTCTAGTGCACCTCCGCTCCCGGTTCTTATGCTCAGCCTCAGCCTCCTGATTAGCTGGGA
TTACAGCGCTGCACCAACCACTTGGCTAATTTTTTTTTGTATCTTTTAGTAGAGACGGGGTTTCGCCATGTTGGCCAGGC
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AAGGAGTCAAAACCAAGGCTCTCTGAGGTTGGAGGCTTAGGCTGTGTTTCAAGTCTATGTGTGTGTAATTCATACAGTGTA
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CCCAGGGAGCCTAAGGAGGGTTGTTTGGCTCTGTCTTTTTGCATGGACTCTGTGGGCTCAAAGAGGGGCTCCTCTGGGAA
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CATCCTCCAAATGTCATTTACTTTTACATTTCAATGTAGGTTATAGATGTGCAGAAATTTAACTTTCTTCTCCGTGAGA
AAGCAGCATCTGACCTAACTCTTCTGTGTAAGTACTTCTGTCTCTCTCTCTGCACTTAGCAGCTCCATCACCATG
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AAGAAATATGTGTGACCTCCTCCACCTTTCTAATATCCGCTTTACCAAAGTTAGCTGCTTGAGGTGGTATATGCCTTTTA
 CATTATTTGCCTCTAAGGGAAAAAATCAAAAGCCCAAAGTTACCTGTTAGAACATAGTCTTGTGAGGTTGTATCTCAA
 GATTTCCCTTTATTCTTGTCAACAACTCAGAATAACTAAAGTTAAAGTTGCTTTATAACCTCTATTATTTCCATCCAAAA
 CTAACATTTCCCTCCCATACCCACAAATTCCTCATTTGCAATTTACCAGTACATTCCTGGATATTAGCTACGCTGCAT
 GAACCAAGGGGTGCAGCCTCATTGTTGTTGTTGTTGTTGATGAGATGAGTAAACAGAGAGTGGCGCTCAGACCTTTAAATGA
 ATACTTGTGGGCAAAATATAAGCAAAATAGCCTGAACCCCCACACCCGAGGCAAAACATAAATTATGGTTAAAC
 TTCCATTACAGAGAACTCCACAAACATGGATTTGATTAATTTGCTGAGCAGTTTCATGACCCCTATGTTATACTTTGCACT
 ATGTAACAAAGAAGCTAAATCTTGAACAGCAAGCTTATTCATGGCAGCCAGCCAGTTTCCTTCTCCCTGTAAAGTCTAAC
 CCTCTGCTGCCAGCAGGAAGGAGAAATACTTGGAGATCTTAGCAGCATGAAAGCCTCTTGTATCATGGGATGTCAGC
 ACGCATGATCAAGGCTGAGGCGGTGATCACCAGGCGCACACTGCTCTTAAGCAGAGGTACTCAGATACGTGGCTGAAAGCC
 TAGCTCAAAATAGCTGCCAGGTGAGCCTCTTTGCTGAGTAGGCTACTCAAAGAACAGCTTTCCCTGCCTAGGGAAGG
 CAGGGCTACTGGCAATAGATCTCCAGCCTAGCAGTGATGTACAGTCATGGTATTTTAAAGAGAACACTTTGAATTTTTCTG
 TTGCTTGACTGTTAAGCCTCAAATTTTTCTGTTGCTTGACTTCTTCCCTGGCCTCCATCCCCCAATCTGCCTCCCTTCAG
 CCTATAAGCAGTACAACATGCTGAACGCGGACACTACTCGCAACCTCATGATCTGCTTCTCTGGATCATGAAAAATGC
 TGATCAGAGCCTCATTAGGAAGTGGATTGCTGACCTGCCATCAACGCAGCTCAACAGGATTTTAGATCTACTATTTTCATCT
 GTGTGTTATGTTTTGAGTATAAGGTAAGTCTGGAGTGGCACAACCTTATACCAGCTCTTATCTCAATTGCAATTTCTGT
 CTTCTTACTCATCCCCCTTTGTTTGGGCTAGGAGCATTAATTTTTCTCATTTCTGTATTCAAATCCATAACCCATT
 TGTAGGTATAGATATGATCATTTTACAGGGAAAGGATCTCTGCCTTCTGCAGAGAGAACCCCAATTTCTGTTGACAGAGTT
 TTGGCCCATAGGATGCTCCAGAGCAGCATCTCAGTGAAGCACATGTCAAACCTTAGCTGGCATCACTGTGGAGTGTACTGT
 TTTGGTAACCTCTCCCATCAACGGAGATCTCACCAAGGACATGTCTCCTACCTCTGTCTTGTCCAGGGAAAAACAGAGT
 TCTGACAAAGTCAGTACCCAAGTCTCGACAAGTCAAGGGATGTCAAGGCCCGGCTGGAAGAGGCTTTGCTCCGCTGGGA
 AGGGGCCAGAGGGGAGATGATGCGCCGCCGGCTCCAGGTGTGTTGGACTGGCCCTCCCTGCTCTCTGTCAAGCAGTTT
 TTCACTGTTTGTGGGGAGGAATGTCTCCCAACATGATAGACACCATTAATTTCTTGAGATATTTACGGTAGTGTCTAGA
 GCAGCGGATTTCTGGGAGTCTGTGTGTGACATTTGTGTTAGCCCTGTGCCTGTGAGGGAAAGCGCTGTTCTACAATTGTA
 GGAACCTGAAAAACAGCACCAAATGACATCTTTAATTAAAACCTGTTGATGGTAAAGGTACCTCTAAGAATGTCAAGT
 CATGGATGAGGTGGAAGGTGTTTCCCTCAAGGCTGAGGCCTTTCTATGTGACCTTTGGCTAGTCTATCCGGAGCATGGTC
 AAGAAACTGAACAGTTCTGGCCCCAAGATCATCTTCTCGATCATTAGGGCACTATTAGAATGGAACCAAGTTCCTGAAA
 TGCTTTCAGAGTGTCCCAGTTCATTCAAGGATTCACCACAGGGAAGTATCTCAAAAGGCTGAGCTTGAATAGAATGA
 ATCCCCAGGTACCTTCAGTCTTATTCCACCATGCTCAAAGTAAACAGAGTACAGCTTATTGTATTGCAAGGGACACAG
 TGGCAGGGAACCTTGGAGGGAGCTCATAGTTTTCAGTGGTGGTCAGGCACCTTCATTTGACACCCATACCTTCATACCCAA
 TAATTCAGTAAGCCCCCAGAGTTTACAGGAATCCTCTGCTCATGAGAAATGTCTCTGACACTCAGAAAGGCAGAGGT
 TCTTCTTATATCTAGTCTATCAATCAAAGAGCGGGCCAACCTTGACATAGGTGTGGCGACTTTGTCTCTCCACCAGCAAC
 CTGCATGGACTCTAATTAGCCCCAGAAATGGTGCTGAGGCTTCTCAGTTGAGCTTGTTATGAATCTCTGTTTATCTTGGGA
 GGGTTTATGCTAATCAAAATCTCATCATCTTTTCTAACTCTAGGGAACGACCGATTTCAGGCCCTAAATGAAAATT
 TGAGATGGAAGAAAGAGCAGACACATTTGGCGCAAGCTAATGAGAAGCTAGATAAGTGAGTCACTCGGCAACTTTCTGCT
 ACTTTTACCTAAAGTCCAAACTATTTTTCCAGGCTGCTTGTATTACTGAAACAACTGCATCCTTCCAAGGTTAGAAA
 ATGAAACATCATTATCTGTGTAATAACAATTCATCCAGGGACCCAGGATAATCAAAGGTATAGGGAGTTGTGGTTTCCAG
 CTCTTAAAAAATTTGTACATTGATAAGCATGTAAAGAAAACTAATATTTCTTTAGCAACCTCAGATGGCTTAATAAAAG
 AGCTGATTTTTCAGGGAGGTAGCAGGGGAAATAGAAAAGCAGGACCGGTGCCTAGGACCGTACTTTCTTAAATCGATA
 TTTCTTTCTTGGAAATATGTACAAGATATACATTCAGATATATTTTATGTGAGTGCTACTTAAAGTTGTTTTTTAAAAATTG
 AAAACATTCTAAATGCTCCAGATAGAAAAATATATTTTAAAGTTGGATTGCCATCAAATGTTTTTAAATCATCTTAAT
 GACATGGGGAAATGCTTATGACATAATGTTAAATGAACAAAGGCAGGTTAGACACTTGGTTTTCTAGTAGTGTGTGGCTC
 ACGCTGTAAATCCAGCACTTTGGGAGGCTGAGGCCGTGGAACACCTGAGGTCAAGTGTGAGACTAGGCTGGCCAC
 ATGGTGAAACCCCGTCTCTACAAAAAATAGAAAAATAGCTGGGCATGATGGCAGATGCTGTAAATCCGAGTACTCAGG
 AGGCTGAGGAGGAAGAGTCGTTTGAACCGGGAGGCAGGTTGCACTGAGCCAAAGATCGTGCCATTCGACTTCAGCCCTG
 GGTGACAGCAAGACTCCATCTCAAAAAAAGGAAAGAACCTCAAATCTCTGATGACATATAGTCAATGTATT
 TTTTAAAGGCTAGAAGGAAATTTACCAAAATATTAATTGCGGTTTTCTTTGGGTGCTGGGAATATCGGTAATTGATGTTT
 TCTCTTTTATACTTTGCTATGTTTCTTACAGTAGATGTGATTATAATATATATTGTTACCAGAAAAAATTTATAAAGA
 AATGAAAGAATAAAAAAACCTGTTTGGATCAAAATCTATGCTATAGATGAATAGATATATTGACGTGTATTGCTATATAT
 GCAACAATTTAGACATATAAGAGCTAAAAAGTATATTTGACTAGATAGCATATGTTTCCGATACCGTTTAGCCACAG
 GATGCCCTAATGATGATCCAGGTTTGTGTGAGCAAAATGTGCTAGAGCTTAAATACCCCTCACACACAGTTGACAAGGTAG
 GATACCCCATGGGTGATGAAGCACCATCAAAGGGGGTATGGGGCAGACTTGATTAGCAGTGTCTGTTTGTAAATAAATG
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 GGGTATGTTTATCTTGACATAAATTCCTGAGCTGATTTATAAAATCTTGGATCGGAGAGTCCATACATTTCTACTTCGG
 GCAATGAAACAACACTACAAAATATGATGACCGGTGGGTGCTACAGAATGCTTAGGTGTTTAGCTCATCTACTCTACTA
 GATTAAGAAAGAACCCCTAAGTAGGCCTGTTTTGCTGGGCTGTGTAAACTGGTGTGTTTGGAAACCTTTCCCTTTTGTCT

TGCAGGAGCAACACAATATTGGTCCTTACCACGCATGGCCTACCGGTTTGCTCTAGGTTAGTTCTCAGCCCTGCGCTACC
 TGGTGGGCTGCTGGTTGTGACAGCTAATGATTCACATCTACAAATTCTCAGGGGCTTTGTGCTTTTTTTTTTTTTTAA
 AGGGAAACCATAGTAAAATTATACTGTTCAACCTACCTACCTGGAAAATTTATAATTATAATAATGGTGTCTTTCACCC
 TCTTTCTGATCATTTTTTCGATTATTTTGGCTCTGTTTCTTTAGAGCAATGATCTCAACTTAGGCTGCACATTAGAATC
 ACCTGGGGAGCTTTAAACCTGTGCTAGTGCCAGCTGCACCTTAGACTACTTCAATTGGAACTCCAGCAGGACCCAGAAA
 TCAGTATTTGGTAAACTTCCCAGGTGATTCTATTGCCACCAATCCATTGTTTTAAAGGAATAGATGGTAAGCTTTTCT
 TTTCTTTTTTTTTTCTTTTTCTTTTTTGAGACAAGGTCTCACTCTGTCAACCAGGCTGGAATACAGTGGCACAATCACAG
 CTCAGTGCAGCCTTACCCTCCTGGCCTCAAACAATCCTCCCACCTCAGCCTCCCAAGTAGATGGGACTACAGGTGTGTAC
 CACCACAACCTGCTTACTTTTTGTATTTTTTGTAGAGACAGGGTTTCCACCATGTTGCCAGGCTGGTCTAAACCTCCTGGG
 CTCAAGTGATCCACCTGTTTTAACCTCCCAAAGTGGTGGGATTACAGGCATGAGCCACTGCGCCTGGTCTAGATGGTAAAG
 CTTTTAAAAAACAGATTAGTGTTAGTGATGGTTGCACAATATGAATGTACTTAACACTACTGAACTGTATACCTTACAAA
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 AGATTTGTGCTGTCCAATACAGTAGCCATTAGCCACATGTGACTATCAAATGCTTGAAATATGGCTAGTTCAAATGTAGA
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 CTAATTTTAAACTAAACTAGCAGTCAATTAATTAAGGATGATAAGGGGGCCGGGCACAGTGGCTCACACCTGTAATC
 CCAGCATTTTGGGAGGCGGAGGTAAGTGGATCAGCAGGTGAGGATCGAGACCATCCTGGCTAACGCGGCGAAACCCCG
 TCTCTACTAAAAATACAAAAAGTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCAGCTACTCGGAGGCTGAAGCAGG
 AGAATGGCGTGAACCCGGGAAGTGGAGCTTGCGGTGAGCCAAGATTGCGCCACTGCACTCTGCACTCCAGCCTGGGCGAC
 AGAGGGAGACTCCGCTCTCAAAAAAAAAAAAAAAAAAAGGATGATGAGGTTAAAATGGTAAATTTGATGTTATGTGACT
 TTATCACGATATAAAAAATTTGATGGCTCATGCCTGTGGTCCCAGATACTCAGGAGGCTAAGGCAGAGCATCACTTGAGCC
 CAGGAGTTTCAGGCTTCAGTGAGCTATGATAGTGCCACTGCACTCTAGCCTGGGTGATAGAGCAAGACCCTGTCTCTAAG
 GAAAAAAAAAAAAAAAAAATTTAGATTTCAATTTATTTTACACATATATTATCACTTGAAAAATGAGAAAAAGTGTCAAG
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 GTATGTAAGCAGCTGCAGTGCCCCCATTATTAGGTAAATGGGACGCAAGAACAGGTAAGTGGTAACCCCTGGCCAGGACA
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 TGGGCTAGCAAAAAAAAAACCATTCTGATTCCTTAAAGTGAACCTAATAGAGGAGCGAGCACCAGGCAATTTCCCATTTCC
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 AAGGACGAAAGACCCACGCACTTGGCTGAGCAACCTCAAGGTGATCTTTGGGAAGTTAAGAGGCTGACTCTCCCTGAC
 TTGGCTCTGAAGCTCCACCCTTTCTAACCAGCCGCATCACTGCCAAGTTCACATCACATCCAGTCTCACTCTCTCTCG
 CATGTTGCAGGGGCTTCCCTTACTCAGATCTAGCAATGGTTTTTCATGCGTGAAATACAGCCATGGCCTGAGGCTTTAG
 GCAACAATCTGAGAGGGGAGCTTAATTGCTAGTAGCAACTAATAACTGCTTCTCTACCCATAGTGTTATTTTTATAATTG
 TCCTCATCATTATTAATAATAGTGGGATGAGGATGACCAGGAACCTTACCTAGACAGTTGTTTCGACAAGACATGAAT
 CACAGAAGGCACCTGCAGTGTAGTTACTCAGGGCCAGTTGCTCTGTTTTTCATTTCAAGGTTGACTATTTTGGAGATTTCT
 TTACACCTTGGTGTATAGATTGCCATCATGGGAACCTGGCCAGGTTTGACATGCGCTTAAATTTGACCTCTTGTGTTTC
 CTAGAACAAGGCCGAGTTAGATCAAGAAGCCTTGATCAGTGGCAATCTGGCTACAGAAGCACATTTAATCATCCTGGAT
 ATGCAGGAAAACATTATCCAGGTGAGGAAAAACAACACCAATCTGATTGTTGGCCATGAATATGTTTACTAGAATAAG
 GACTTCTTTATGCAAAATTTGTGAAAGACATAAATGTGATCCCATAGTACCTTTTTTAAAAAATGAAGTTGAGAAGTTTA
 CTATTTACAACAGTGTCTACCTTATAAATTCAGAGATACCAACATTTCTTGGCTTCTTTGACTTAGGGCTTACTTGG
 AGAGGGTTAGGTGTTTGGCCAGCTGACCCCTCTGGTTAAATCTGTGTGAGTATGTACCAAGTTTATAATATCGGATGTTGG
 GTTTATCGTTTAGTATCTAGAACAGTAGTGGTAAGTAGAATTTTTTCTGATGGGTCAACTCCAGTTGAATGATGGTCACT
 GTCTGATATGGGAGCTATGATTATGACTAGGCTAGGTAAAAAGAGTGCTAAATTTGACAAATGATGTCTTCTTGGACTT
 AAATTTGTTAAGGAAAGTCATTTGTACCATGAATTTGCCATCCCTGCTGTAGAAAAATATAGCTTTGTGAACTTTGTACC
 ATACTAATTTTATCTTCTATGTGATTATTTCCACAAATTTCCAAGCTGTCTAGGTAATAATGAGTTTTTAATTACCTGA
 AAAATGAGTTCTTACATGTTTCCATTGAGAAGTCATTCATTAGAGTAGGTCCAGGATTGCTTTTAGGGCTAGAAGAATA
 TCGTTGAAACACAGTGAAATCTTAATCTCTAACTTTTGAAATGTCTAAATCAAAGTAATCATCATACAAAAATAAACA
 CAAAAAGTATGTGATATTTTTGTGACTTTAATATCTTTGATAACTTAAATGCTTGGTATCACATTTACCTTATCTTTAT
 ATAGCACAATATTAGGTGCCAAATATCTATACTAGCCCCAAATATATTTGCAGTTTTTCAAAGAAAGCTGAAACCTTTG
 TTATTATCCTTGGTGTGTTAGTCTTCTGTAGGTGATAACAAGCTTCTATTTAGAAACATTGCTGCCACCAAGCAGCC
 CCTGTTGTACTGGGAAGCCCAATTTGTGTTTTGCATCCCATAGGAAAGCTATGTCTTGATACAAAGAAAGAACTTTC
 CAAAAGATGTGACCCAGGATGAGGAGATGGGCTTATACCTTCAATTTAGGAACCCAGAAATAGGTATAATCCCAACT
 CATTGGAAGCATTGAAATAAAGCCATTGGAATAGGTCTTCAGTTCCCATGGTTAATGGATGATACCCATGGTGGCTCA
 CCAACTCTTAAGACTCACCCTGGACATGGAACATCAGCATTACTGAGCTAATTTGTCAGGAACATCCAGTTCAATTGGCA
 CAGTGCAGGGATTCAATGATGCTGTTCTTCCATTCCCCAGCGAGCTCGGCTCTGGACTGTAAAGACAGCCTGCTGGGA
 GGTGTTCTGAGGGTGTGGTGAATTTCTCTGAAGTGTGATCAGAGTACCACCTACCTGACTCACTGCTTTGCAACACTCCG

FIG. 7B (6 of 15)

TGCTCTCATCGCCAAGGTAAACTTGGGATGCTTGTCTTCTCTTAATTAAGAGTAAGATTCTCATCTAGCTTCATAC
TTCTCTCTTCAGGTGGACAAAAGTCACAGAGCATATTAAGTGGCATCACAGTAAAGGTCTTAAGTCTTCTAGGAAGAA
AGCAGATGCCCTGATTCTGTGGGAAGCCACCATGGAGAGGAAAAGCAGTGGCTCCCATATTTGAAGTGTGGACCTAACTC
TAGAAGTTTAAATGGCCATTGCTGAAGTCTATGACATGAGAACAGAGATCAACTGAGTGACTTAGCAATTTCACTCT
TTCTCTGTAATACCTCTGCTGAGTGAGATTAATCCTCTATGTGACGCCCATTAGTCTTACAAAATGTCATGCCATAAAA
TGCCAGGAAGGTGAGAAATGAATTTCTACGGCCTGAGGAATGAGGATTATCTGGGGTAACATGCAGATTATTTTCCC
TTTATTTATTTATTTATTTATTTTGGAGACTGAGTCTCGCTCTATCGCCAGGCTGGAGTGCAGTGGTACCATCTCAGCT
CACTGCAGCCTCTGCGCCCTGGGCTCAAGCGATTCTCATGCCCTCAGCCTCTGAGTATTGGGATTATAGGCGTGTGCCAC
CGCACCAGCTAATTTTGTATTATTAGTAGAGACAGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGACCTC
AAGTGATCCACCTGCCCTCAGCCTCCCAAAGCACTGGGATTACAGGCGTGAGCCCCGTTCTCGCCCTATTTTCCCTTTA
TTGAAGATCTCAATTGGTGCCCTTCTACATGGGGCTTTTAAATTTAAAAAGTAAATTTCTCTGCTCATCTTCTCAGGA
CCATTTTCTCTTCTTCTCATCACCAGTAATTTCCAGGAACCCAAAGAACTCAGGTTTCCCTCCATCATAGTTGTGATTTC
ACCAGTGAATGCGACCTGGCTCAGAGTGCAGTTGATAACACAGCTCTGACCTTTTAGCTGGACAGTTCAATTATTAATC
TCAAGTCTACTCCATTGCTTAAATCCATCTTCTGATTACATAGCTCATTATCTTTATGGAATAATGCATTAACTCTTCT
AGGCTTTTGTCTGTCCAAATGGACATTTGCATATTTCAACGGTCCAGAAAGTGTATCAAACTGCCAAGTGATGCCATAAT
GGCCCTTTATGTCTCTCTAGTTTGGAGACTTACTCTTTGAAGAGGAGGTGGAACAGTGTTCGACCTATGTCAACCAAGT
CCTGCACCACTGCAGCAGCAGCATGGATGTACCCGGAGCCAAGCCTGTGCCACCCTTTACCTCCTCATGAGGTTCAAGTT
TTGGAGCCACCAGTGTAAAGAGTTCAAACCAGCTGAGTGACCTGGAATCAGTAGAGAAAAATTGATGTAAAGCATCAGCTG
CGAAAAAAATAAGGAAATTTTGCAATATTGCAGTTTACTTCTGTCTGTGAGAAAGAAACAATTGAGTATGTAGATAGA
TAGCAGCTTCCATTTTAAATTTGCATCTAAAAGTGAATTCATCAGATAAATGCAGTGGTCTCTATCAGTGTGTTCTAAAA
TAGACAGCCAGGGGCCAGGAACGATGGCTTTACCTATAATCCAGCACTTTGGGAGGCCGAGGTGAGTGGATCATTGTA
AGTCAGGAGTTCAAGACTAGCCTGGCCAGCATGGTGAAATCCTGTCTCTACTATAAATACAAAAATAGCCAGATGTGTTG
GCGCATGCCTGTAATCCAAGCTACTTGGGAGGCTGAGGCAGGAGAATTGCTTGAACCTGGGAGGCAGATATTGCAGTGAG
CCGAGATTGCCCCATTTCACTCCAGCCTGGACAACAGAGTGAGACTTCATTTCAAAAAATAATAATAATAATAATAATA
ACCAGGTGCAGTGGCTCATGTCTGTAATCCTAGCACTTCGGGAGGCCAAGGCAGGCAGATCAGATGAGGCCAGGAGTCCA
AGACTAGCCTGGCCAACATGGTGAAACCCCGTCTCTACAATACAAAAAATTAGCCGGGTGTGGTGGCACACACGCCCGT
AATCTTAGCTACTGGGAGGCTGAGGCACGAGAATCGCTTGAACCCAGGAGGCAGAGTTGTAGTGAGCCAAAGATTGTGC
CACTGTATTCCAGCCTGAGACCTGTCTCAAAAAAAGAAAGAAAGAAATGGAAGAGTATTTTAGATTAAAGTT
ATCATCTGTGGGGGAAAAATAACAATAGACAGGTTAGAATTCAGAAGAGTGTTCCTGTTTCTAAATTTCTGACTAGCTAG
TGCCAGAATGACCTGTGGAAGAGGATTTTAAATGATCGGTGTCTATTAACCTGAGTTTTATTTTAAATATTTTATTTATTT
ATTTATTGAGACAGTGTCTGTCTGTCAACCCAGGCTGGAGTGTAGTGGCACTATCAGAGCTCACTGCAGCCTTCAACTC
CTGGGCTCAAATGATCCTCCTACTTCAGCCTCCCATGTAGTAACCTGGGATTACAGGCACGAGCCACCTTACCCAGCTAAT
TTTTTTTGCAATTTTGTGAGACAGGCTCTTGCTGCATGCCAGGCTGGTCTAGAACACCTGAGCTCAAGTGATCTTCCC
TCTCAGCCCCCAAGTACTGAGATTATAGGCATGAGCCATCCTGCCTAGCCAAGACTTGAGTTTTATTCAAAGCTACG
AAGACTTTGGAGTTCAAGCTTTATTATAGAACAGTCAAGTTTGTCTTAGTTTGTCTAGATTTTGATACCTTCTTTGGAATT
TCCATTTGTGGCCATGTTAATAAGTATGCTCAAGTGATATATAAGATAAATTGGCCCATGGAAAAAGTCAGCCTCCTC
CAAATGTATTAGGGATGATTATTTAAAGACATTCCTCAGGGGACCTTGAGGTAGCCATGTTTTTCCATGGGCCTGTAA
GAAAGAAGAAACAAACCTTGTGCTTACCCGGAGTTCAAATCTCAGAAATGCTGGCCACAGAAGTCCCTGATTATTT
TATTTAGAGACAGGCTCTGCTCTGTCAACCGTGGCTGGAGTGCAAGTGGCGAGATCTTGGCCCATGCAACCTCTGCCTAC
CAGGTTTTAAGCAATTTCTCTGCCTCAGCCTCTCGAGTAGCTGGAATTACAGGTGTCCACCACCATGCCAGCTAATTTTT
GTATTTTTTAGTAGAGGCGGGTTTTGCTGTGTTGCCAGGCTGATCTTGAACCTCTGAGCTCAAGTGATCCACCTCCTT
GGCCTCCCAAAGTGCTGGGAGGCTGAGCCAGAAGTCCCTTTCTTTAATAAAGTTTAAATAAAGTCCCAAGAAGAACTC
TTGGCACAAAAGGATATACTGTATTTCTGGACCAACTTTATAAGAATCTTCCAGCTTGACAGACAAAGGCAGCCAGTC
CTCAATGAAAATTTAAAGGGAGCCTGACAGATTTATGTGAGAGCAATGTCCATTTAAACCATTAAACAACAATATGAAT
GTTGTGCAAGTGATGCTCCCATTTCAATTGAGAGAGAGGAAATAATTAAAGCGGGGCAAGGAAACACTGAGGAGTTGT
TTGTGTCTGGCCATGCTGCTTTCAGTTATCTACTGCTAAGTGTGCTTATTTACTTCATCTTTTTTTTTTTTCTACTGA
TGCAGAATTTTGAAGAGTAAAGATGCAAGTAACCATGTCCCTGGCATCTTTGGTGGGAAGAGCACCAGACTTTAATGAA
GAGCACCTGAGAAGATCCTTGAGGACAATTTTGGCCTATTGAGAAGAGGACACAGCCATGCAGATGACTCCTTTTCCAC
CCAGGTACACCGAAGCACATACCTTGTCTCATGCATGAGTTTGGGATCTGCCAACTATTGTGTATGTATGTATGTACATA
TATACACAATTTATATATAAATATATAACATTTGCAAGATTTTATTTGTTTCAATATGCATGTGCTCTCAGCACTCTGAGAG
GTTTTTAAAGAAATACATCCATCACTGTCCCCAGTCTCAATATGCTAACAGTCTATTTGGAGTGCTCAGTCTCAAAACA
ATTAGGAGGCAGTACAAGACAAGTGATACATAAGTGCAAAGTGTGTGGTAAGGAGCTAAATGCTATGGAAGGTTAGAGGA
AGAGAGGTCTGATCAATAAACAATCTGGTGGCCAGGAAAGCCTGCAGGGAGGGATGACACTAAAGGCTGGGGTAGGATT
CCGCTAGGCAGGGGAAAAGTGAGGGGGAAAATTGTGAGTAGTTGAAACAATGAATGTTTGTATCTGTAGGGATGGTAAAG
GGACCAGCTTGTCTGGTGAGGGGTAAGGAAGGGCCAGTTTGAGAGAGCTTGTAAACAAGGTTGTCTTAAGGAAATGTGT
AAGGACAGTCATCTCTTCCATGTCCATTACGATACCGTGGAACCTTAGCCTGTCCATTGTCTTTTAACTCCAGCTCC
TAGCCTGTCTATGGTAGGGTCTTAATTAAGTGAGAATGAATGAATGAATGTTTCTTTTATCCCTTAGTCTGAGAACC

FIG. 7B (7 of 15)

CTATTTCCGGAGTCTGTTTTGCCCTCTCGGGCAATGTTGCATCCTCATTCTCAGAATCTTTTCCCTCTCCTCTACATCAA
 ATCGTTCCCTCTCTCATTTTCATCTTGACCATACTCCTTTAGTTCCATCATTTATATAGAGGTATTCACCAACAAGACCAAT
 CAAACTATGGGCAGTTTAAATAAAGGTCTTCAGTGCCTTCACCCAATGAAATGACTCTAGTGGTAGAAATTTTAGGAGCCC
 TGGCAAGCTGGCAGAGGGGAACGGGGATAAGACAACATTCTGTGGCTGAGTTACCTGCCAGGGTCTCTAGATCAAGCCAT
 AGTCTCTCCCTGTTTTTGTACTGCAGGCTCCCTGGACCTCCACTGTTGGTTTTATAATTAAGAAATAAATGATTACAAGA
 GGTTCTAAAATCTCTGAAGCCCTGGGAAGATCCAGGAGGCTTCTGAGACATGGAACCTCAAGCTGAGGTCTAAGCTGCTT
 CCTACTTGGTATAAAAAATCCCTGATATTCCAGAGTAGAGTTTGAACCTTTTCAGGTTACAAATAACTGAAACTGGTTCAA
 ACTAATTTAAACAAAAATGTTGGAGATAGAGATAGTATGAGGATTCAGGCAGATTTCTGGATCTCAAGGGCCAACACACA
 TCCAGGTCTCATAACTCCTGGGCTGGCGAAGATGAAACTACAGAGTCAGGTCTAGATGACTCCGCCATCCCTAGTCTC
 TGCTGCCCTCTGATCCAACCCCTCCCATGGCTTCCCCTTGCAATTTCAATGTAATCCTAACTCTTCACCTGGGACTACAAA
 GCTAAGATTATTTTGGGCTTACACTTTTTTGCAAGTGGAGGAACCTTCTGTAATCTGAATAGCATCTTATATGACACAG
 TGAATAAGAGGAATTTTCAAGGAAGATCCTGAGATGCTTATGGATCTCATGTACAGGTAAGCTTTCTGACACACTCAAGG
 GACACCATTGTTGGGCTCGAGGATTTGTCACTGTGGAGTTCTTACTAATGTAATGATCAGCTAACATGGATATAGTGAT
 TTGGATGATAGCCAAATAATATATAGAAATTAACATTTCAGAGTAGGTTAATTCATATGTAAGTTTTTCAAGAGGATCTCC
 CTAATTTAAAGTGAAGCATAATAATGTTATTAATAATAAACATTATTAATAATAAACACTATCTTCTACTTACCAC
 AGAATCAGAGAAAGAATAATTAAGTGTATAGGAATTTTCCATATGCTTTTGTTCGAATTATATTCAGACATACATA
 TATAGTTTTTGTAGAAATCATTTTTTACGGTAGTGTAAAGTTGGTCTTCCAGTCCCTGTTTCAGGAGAAATTTACTTA
 CAGAGGCAAAATTTCTGTATGCAACATCATACAAAGGGCAGTACTTTTGTCTTCTGTTTTATTTTGAAGAGAAAGGAAAG
 AAAAGGCAGAAATTTGCTGAGAGCCATTAATAATAGACATCATGTTATCAGGTATTTTTTCCCCATAAGGCTTTTACTAA
 GTACTATTTCTTGGAGGTGAGCAGCTTAAACATGGAATAAAAATAGTTGGACTAATAAATGTTTTCTTCTGTCTCGTT
 TTCTGGAAATATAGGGCAAAATCTCAGGTGGAGGGGTACAGGGAACCTCTTGGGGAGAAAAAAGAAAGGTACACAAAAG
 TAGAAGAACAGTGTCAATTAACCCACTGTCTCAAACTACTTCTCACTCAATCTGTCTTCAAGATTGCAAGAGTTACCA
 GGCATCTCCTGATCTGCGGCTGACCTGGCTCCAGAACATGGCAGAGAAACACACCAAGAAGAAGTGCTACACGGAGGCTG
 CCATGTGCTGCTGTCACGCCGCTGCGTTAGTGCTGAGTATCTGAGCATGCTGGAGGACCACAGCTACCTGCCCGTGGGC
 AGTGTGACGTTCCAGGTAGGGTGTGTGACGCTTTTCCCTTAGAGCAGTGGTTCTCAACTGGGGCGATTTTGTCCCCCAGC
 CCCAGGGACATTTGGCAATGTCTAGATACATTTTGGTTATCACAACCTGGGATGGGTGAGTAGGTGCTACTGGCATCTGA
 CTGGTAGAAGCCAGGATGCTGTGAAACATTCTGCAATAGGAGAGCTCCCTTGACAAAGAATTGTCTGGCCCCAAATGTCT
 GTAGTGCTAAGGTTGAAAAATCCAAGTTCATACATTACATTTGCTTCTTCTAATTGCTTTCCCATCGTCGTTGGGTTTT
 TTTTAAATTACTGTTTACAATAATGGCACCTAGCCATTATTAATAGCACTTTAGGAGACATTTGCAAAACATTTACATG
 CATGGCTTCATTTGAACCTCCCCGTAAAGCTGTGAGGCAGGTAGGTAGGGAAGGCGGTTATTATTTCCCACTTCGCGGATG
 AGAGAACTGAGAGAGCAAGTTTTCTAAGGTCACTTAACTCTTTTTCAAAGACTGTAGTTGACACAGTATACTGACATT
 GTGAAAGTTTGGAAACATTGGATAAATGATTTTCTCCTGCCCCATTCTATTGATTCCACTCTTCACTTTTATAGGGGC
 CCCTCTCCAATCCAAAAATCAAGAAAGAATCAAATTGACCTGAGAAAGGAGACAAAAGGCTGAATCAGTACCTTCTTAG
 GATAAGCTGAAAATTACCCACATTTGGCAAAGGGAATTTCTGCGAGACCTAAAGCTGGCTCGGATGGGGGTCAG
 TGGCCACTTAAAGTGTCTTCTTACTGAATAGTTTAAATAGTCTTTAGAGAGAGAGAAAAATAAAAAAGCACAATGTTGGGTACT
 TTTTTTGTAAAGAGACATAGTTTGTAGAGATGACCATCCCTGAAACCATGAACAATATAGCTACAGTAATAGAGTGTTTTT
 CAAGCCAGACTCACGAAGTCATTTACAAGGGTTGTATTATCTTGTGTTGAATTTACATGGCTGATTTTATGAAAAGCTT
 TGTCTTGTATTGTTCTTCAACACAATTTTGTGATGTTGTATGAACCAGAAAGAAAGAACATTCAAAGTAGCTTCCCC
 AGGCTTAGAGAATAAGTCACTGAACTATGCTGGTGACGCCAAGAGCTTCTGGTTTTCCAGAACACAGCAAAGCTGGGTA
 TTGCCCTCTATGAATAACTCCTCCTTTCTTATGGTCCCTCAAGAACAAAAATAGTCATTCTGTGATTTTCTGCTTGGCAAA
 TGAATTTTCTTCTTAAATTCAGAAATGTTTGTATATAAAGCTGATAATTAATCTCATCCAAAAGCATAAAAATAACACCT
 GATTTCAAATCACATAGAAGTGTAAGAAAGTTATAAAGTTATTTTAGATGTATTGCTTCTTTTCTCAAATTTATTT
 TGACCATGTGATACATCAAAAAATAATATTATAGTACTACTCTTTCAATTCCCAGGAAATTTGAAGGTTTAGCACTTCA
 TATTGTTTCATTTACTAAATTTATTTTATCTTCTTTTATTCCTTTTCCCATGACTATATTTTATTTTATATTTACTT
 AAATATCAATTGCATTTTCAATTTGACTTTTATATTTAGTAAGCCTTACTGTTCTAATTTTACCTAGAATTCAGTTGATT
 TGCTAATAATGACATGCCAAAGTGAATCATTATTACACAATCAACAGAAATATTCCACATTATTCGACATGGGGGCATA
 CAGCTCTATCTGTTACATATATTTATCCATTGATTCTTCTTTTAGAGAATATTTATTGAATACTTATTCTGTCTCAT
 GAACGTTACATTTCAACCAGAGAGACGTAATATACTAATTTATCCAATCTTGTTCAGTTATAATTATGAGAAATACTG
 TTATAAAGAGGCACAGATATTGTGAGCATTTATGGTCCAGGCCCTGTGGGTGAGGGAAGGTTGAAGAAGGTGAAAAGGA
 AGGCAGAAGAACTGAAGTGTGAGGGCTTCTTGATGTAGAGGAGGCAATGAGTTAGGTGTTGTGAGCTACAGAAGAGAAG
 CCAAATTATATTAATGTGTATGAGTGAATTTCTTCTCAATGGGACATACCAAATCAATTTGGAAATGTAGCTGG
 CAAGTGAAGGACACCAACCCAGACTGACAGAAGGTAAAAATGGAATTTATCAGCCCGTCTGAGGAATGTGAGCCTGGA
 GTAGCACCTGCCATACTGGACCTAGGGGCCCAACAATGTCAGCAGAGCTCACTGTCATCACCCTTCCCATCTCTGCCA
 TCTGTTGTGTGAGCTTCACTTCTCAGGCTTCCACACCACAGTTTAGGTTTACATCTCTAGGTTCAAGTCTAGGAGAG
 AAGAGAGATGCCTCCTTTCTAGCAGTTGCAGAGAAAGCCTCAGTGCATCTTACTGATCCTGTCTGAACATCTGATCCTGT
 GCTCATCCCTGAACCAGCCATACTGGCCAGAGAAATGGAGTGCTCTGATTACTGACCCCGGCTCATGGTCCACACCTG
 GAATTATGGGTGATTTCTTCCCCTAAATCAGGATGCCTTACTTTATAGAAGGAGGAAAGAATTCTAGACAGCATTAACAA

FIG. 7B (8 of 15)

CAGATGTCCAGTGTGATTTTGCAAATGCTCTGTGCTTTAATTTTCAACCTTGTCTGCTCCAATGAAATAGAGCTTTTG
GAAAGATTTATAAACTAGAGATAAAATAATATGTGCAAGGAAAATAACTTTGAGGTCACTGAATTCAGGAACTGAGA
TCACTGAAATTCGTGTGTCAGAGTGAATATTTATTTTCACAACTGTAGATACGGACACATTCTTAGATACTGCTGTAC
TTGTACCTCCCTGATCCGGAAGCCAGAAAGTCTGCAGAATCCTTTTCTCTGACTACAGCTAATGAGGCTACATAGCTT
CAAATCTGTTCTCTAATGTGGAAAATTGCATACATTCTAATAGTATTAGTATCTTGGGTTATTAAATGCTTCACTGA
ATTTCTTGGATCTTCTGTGTGCACAGAAACATCATAATACATAGGGCAGGTTTGGAAAGAAAGACTGGCCACAAAGGCTTT
GAGAGCCTCCTCTATATTTCTAAAACTACGTTACAGTATTGCATGTGAAGAGATAGGGCTATCTATGACAACTATGTCC
TGACTGATTGCTAAGGTTGATTACATGATCTTGCTAACCAGGCCAGAAGGCAGACAGCTTTTAGTTTACAAGCCAACTC
TGATCAGTTAGTAGTGGCTGACTGGAGAATATGCTTAAGAATTTTCGAGACTATGTCCAAGCTCTGGGGAAAAAGTGCTA
CAGTTGATTAGTTATGCCCTGCCATGATTACAGCAATAGGAAGGAGTGGCATGTGTGCCACCTGTTTGTAAATCCCTAACT
GGGAAGGTTTCCCATTTCTTCTGTTTTTCATATGCATTTCTTCCATAGCTGTGAGCTAGGAAGAAAATGATTCTTGACCT
GTCACATATTTCACTGCCAGGGCCAGTGCTAGGGTGAAGAGGCACTCACCTCAGGTCGAGCGGGTACAAGATCAGTACT
TCCATGGCCCTAAAAGCGAGTACCTCTCTAAATTTTGTCTTGGGTTTCTCATTTGGTTTACCCCAACCATGGTCTCTGCA
TGCTCTGCTAGAGGCTCTAAACGCAATAGTTTATGTAAGGAAACAAAATGCATGGAAACAAAATGTTTACGGAAGAACAAA
AACACACACACAGTAACCTGCTGCAATGCCATGAAAACCTTCTTAATGAAGACAGCCTCGCTTGTCTGTGTATGTAT
GGCTGTTTATCTGAGTCAACTCCAGAGTAGCAACATACTTCAGAAAAACACCACTGTAAGTCAGAGGTCCACTCGGTGAA
ACAGGGAGCCTAGTTAATGTTAATTGGGTCTTTGCCTTTTGAAGAACAGGACACAGCCCTATGTCCCTTAGGGTTGTTT
CACTAAAGTAACCTCAGCTGTTGTGACATTGAGGTAAAGTGCTCTTTATACAAAATCTCCTAATGGTTAAAAAGAAAAACGT
GAGGTTTGAAGACCAGTTGCTCAGTGCCTCTTCTAAATGAATGGCAGACAGATACTCTCGGGGTAGAATTACAGACCT
AGTTTAGTCACGGTCTTGGTAAGGATCTGCACACCACTCTCTCGTTTCCCATTCGGGGTTCTGTGGTCTCTTACTAG
TCTGGTCGCCCTGTTCTCCAGGCTTATACTGTGGTCTCTTTCAGAATATTTCTTCCAATGTGCTGGAGGAGTCTGTGGTC
TCTGAGGACACCTGTACCTGACGAGGATGGGGTGTGCGCAGGCCAGTACTTACCGAGAGTGGCCTGGTAGGCCCTCCT
GGAGCAGGCCCGGAGCTCTTACGACGGTCTGCTGCCAGAGGCGATCCCGGGCTGGCCTCCCATACTCCAGCTGGAC
TTGGGGTGTGGAACACCTGGTCTTAATGGCCAGTCAAGCCCACTTCCCAGGACACGTGCCAGGGTGTGCGGGGACAG
GGGATGGGCCCGGGAGGACTTTGATGTATGCAATTCATGAGCTTCCAAGGGAGCTGAGATAACCTTTCATCACAGT
GCCGATCTGAGCTTCACTGTATGCTCATTGGTTGGGCAGCAGTTTTCAGATATTATTTCTATTAAAGGGTGGAACTA
AGCCACAGAGAGGTGAAATGGCCTGCCAGGGTTACACAATAAATGATGAGGCATGTTTTCACCTCCCTCGTTTTCTCT
CAGAGAGAAAAAATAGGGAGGAACCACTGGGAGGAGAGAGGAGGAATACACAGACAGTGTCTTCCCTCTAGCCACTG
TGAGTCTGAAGGACATCACAGACCAGGACAGCTTACAGAAATGTGGGCACAGAAACCACTGAGACTCCTCTGGTTAA
CGTAATCTGGATCTAAACACTCCTAGTATATATACTAGAAAAATATATAGAGAGATGAAGTCATTGAGATTACAGGCAAA
GAGGAAACACTGTGTCTATTCTTTCTTTTGTGAGACAGAGTCTAGCTCTGTGCGCCAGGCTGGAATCGAGTGGTG
CAATCATGGCTCACTGCAGCCTCTACCTCCAGGGTTCAAGCAACTCTCTGCTCAGCCTCATGAGTAGCTGGGATTACA
GGTGTGCACCACCACACTCGGCCAATTTTTTGTATTTTTTAGAGGAGACAGGATTTACCTGTGGCCAGGCTGGTCTCA
AACTCCTGGCCTCAAGTGTCTGCCATCTTGGCCTCCCAAGTGTGGAATACAGGTGTGAGCCACCACGCCCCAATT
GTTTTCATTTTAATAATCTCCCTCCTCTTACATTTTAAGCCAAGAAAGTATTAGTACTTTACTATATTTAGCTGACC
CAATTTTGTCTTCACTATATACTATACCTTATTTTCCAGTTTTTATTTCCAAAGTTTCTCTAGCAATTTATTTA
TTTTAATTATGTTTTAACTGTCTCTCTCTATTCTTGTCTTCTTTTCAAGATTTCAGAAAATGTCTAATATACTCTCAT
TTTTCTCAAACCAACAAAATGAATAGAATCCTACTAATCTTTGGAGGCATACATTTAGCATCTGGCTAGAGGAGGA
CCTCTGATGAAATTTAAATATACTAAACTGCCTTTCTGAATTGCTGTAGTCCCTGCTACCAAACTTCTCTCTGTTTT
TTCTTTTCTGTTTTGTTTTGTTTTGTTTTGTTTTGAGGCAGGCTTGTGCTTGTCAACCCAGGCTGGAGTGCAGTGATG
CAGCCTTGGCTCACTACAGCCTTGACCTCCTGGGCTCAGCCTCCACCTCAACGCCCAAGTAGCTGAGGCTACAGGAGC
ATGCTACCACACCTGGCTGATTTTTTAATTTTTTTGAGAGATGGGGTCTCCCTATGGTGTCTAGGATGATCTGAACCTC
TGGGTTCAAGTGATCTCTCTGCTCAGCCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCACTCAGCCAGTATTT
TTTTTTCCCCGAAAGCTCTTCTCTTACTTATCGCCATACAGGACTACTTAGCGAGGTGTCTAGTTTCAAGGCT
ACCACTGTCCCAAAAGTGTCTAGATACCCCTTCTTGCCTGTGAAATACTGTGATACAACAATAAATCACTCTCCAGCA
CATTTGTTGGACAATGACCTCTGGTTGTCTTCTTAAGTTTCCAGTGGATTAAATCTCTCTGATGCTCTTCTCTCTTT
CCAAGGGAGGCTTATATGAGACAGTTAATGAGGTCTACAAGCTGGTCACTCCCATCTCTAGAAGCGCATCGAATAATCCGG
AAGCTGACACTCACTCACAGCAAGCTGCAGAGAGCCTTCGACAGCATCGTTAACAAGGTAGCCGGGGAGCCTGGCTGGCA
GGTCTGTACCTGGTGGCAGGCGACCTGTCTACAGATGCTTAGCCATCCTTCTCTCCAGGGAGTGATTATCTTTA
GCATATTGCTTTTGTCTCTACCTGTCAAACAGAAAAGGGCTGAAATTTCTTAACAGAGGACCAAAATTCATATGTGAA
AACATACAGCTTAAATTAATTTATAACCAGGAAATGTGAGAAATTTTAAAGTGAATTTAAAGAAAGTCCCAGAAATCTTT
CATGGGATTTCTTTTGTGTTTATTTCTGAAGTTTATTTCCATTAAGCATTAATTTTTTTAAGGAGTAATTTCTGTTTACAT
CAGCCATAGGAGTAAAAATGCTTTGTTAAACAAATGAGAGACCCCTGCCTTTGCAACTCAGTGGCTCCTCAGGATGACAT
AACTAAGGAGAGCTTTTTATATTTTGTCTCCTCAGGATCATAAGAGAATGTTTGGAACTACTTCCGAGTTGGTTCTTTG
GATCCAAATTTGGGGATTGGATGAACAGGAGTTGTCTACAAAGAGCCTGCAATTACCAAGCTCTCTGAGATCTCACAT
AGACTAGAGGTAAGAAAAGTATTCTGTGCGCTGACCTGGTACACTTTACAAAACAAGTTAGAGTGGGTCACTACCAA
AAATAACAAATAAAGAGTTATGGATTATCATTTGATCTCTACATAAAGTTTCCCTTTGCAATTTATAAAGGCAAGT

FIG. 7B (9 of 15)

AGAAAGGTATTAGGTGAGATCATGAGGTGATGTAATATTTTGATAGTTTTTCCCTAATACTCTGTGTATGCTTTTCACAG
TTTGGAAATTTTATATGTTGAATATTTATTTTGAAGTCTGTGCAAAATTCATCAAGGTCATGTGCTTTCTTATCACCTT
TCCAAATATTAGTAGTTTATACTAGTAGATAGAGAGTAGTAGAGTTTTTCAACATGAAGTTTAGCATCTTGACTTTGAAG
TAATCTAGCCAAATGACTGAATCACCCCTAGATAATGGTGAGGCCATCCTTTAGGTATCACTGGATGGCACCTGGGGTCC
TTCTGATGTGGAGCTACTCAGCTGTGGCCAGCCCGGCTCCAACCTGCCAGTGAGTGACATTTGGTCCATAATACAACAGA
AAAGTGTAGCATGTTGTTAGAAGCAAAGCTGAAAGCATGGAGAAAAAGAGAAACAGCCTAGAGAAAGGTCAGGACAAAAG
AAACACAGGTTATAAGGGCCAAACACTAAGAAGCTCAGTCAAAGGTGCCCTCCCGATGGGATTTGGATGAACAGGAATTTG
TTTACAAGAGCCTGCAATTACCAAGCAGGACTGGGGTCTTTGAACTGCTCACAATTAACCAAGATTCACTCCTTAGG
CTTTTCAATTGCTTTGAATTTGTGCCCTCCTATGAGTGTAAGCTTAAACATTTGTGTGCTTAATGGCTTCGTACACTCT
CCATCCATGCCAAAAAGACAAGAGGGTTTATCCTTACTTGACTCAAAGAAGCCATTGCCAGGGTGGCTGGGTGAGTTG
CCCCAAATTTGTTTAGCACATGAGAAAAAGAGCTAGCAATTGACCCAGTCCACTTGGTTCCCTATATTGTTTCCCTTAC
TTAGAATTAGAGGTATATATTTTATCTTCTTGTGCACTGTGATTTGCCACAATATGGGAAGGCTGGTGAATTTCCAAGTTT
CCAGGGTACAGAAGGCGAGAAGTAAAGAGTGTGATACCCAGGAGATACCTCAGCAAATATAATGATGTTAGCTGAATTA
GAGGCCAAGCATACTCTTATAGGGAAGCATATACCAGTTGACAGTGCTATTTTTATTTTTGTCTTAGGAAATGCTGAAC
TTTGTCTATTAGTCTCAGAGGAAGTCTCAATAATCAGTGAACATCATTCTACCTTGCACTTGCTCCAACTTATTTCACTT
CCAAGAAGACAAGAGATTGCATTATGTTAAAAATAACCTTTATAAACTGTTGGTCTTCTTACCTAGGCATTTTATGGTCA
ATGTTTTGGTGCAGAATTTGTGAAGTGATTAAAGACTCCACTCCTGTGGACAAAACCAAGTTGGATCCTAACAGGTAT
ACAAAATTTTACAAAACCTAACCATCAAGCTCTAAATCCCTTCGTTCTCTACCCAAGAATACCTAATGATCTCATCTATC
TGGACTCTCCAAGTCACTTAAATGCAGTCAAACCTTTTCGTCTAGAGTTCAACTACTAATTGGTCAGATCTTAAAGAAAA
TATAGTCAAAGGCAGGAATCATAATAGGAGCTACCACTTATTAAGCACCAGTGTGTACCTGGAAGTGCATTAGGCCCTC
TACATACATCATTTTATTTTATCCTGCAACGACCCCTGGAAGTAGATTTTGTCTTCTATTTTAGAGATGAGAAAACCTG
AGACATGGAAGAGTCAAGCAAGTTTCAAGGTGATGCAAGCAGCAGAGCCAGTACTCAGACTTGAGGTCTGTGCTTCTGA
ACCCCTACTCTTTCAGCACTGCTCTTTACTGCTTTTATAAAACCTTTAACTCTCCATTTCAAACCTCGACACACTTAG
TGGCTTCTCTTCTTAGGCTGCAAGTATTCCTTCCATCCAAGTCCGGGATCACTGTGCTGTTGGGGGAATGGTAAAAACGG
CTTGGGTTTGGGTTTCTCACTTTTACAAGAGGGTATGTTCCATTTTACCCCAAAATGGGTGTACAGTTCTGTATGCTAAC
ACGTGGAGGTGGTATCAGCTCCACAGGGTAAAGGCTCAGTCTCCTCAAGACTGCCCTGACTTCAAGATGCCAGCTTCAA
GAGGGACCCCCAGGCCAGCCAGCTTCTGATCAGCCAGCTACAAAATTTGGGAGTTTCTATAACCTGTTAGCTTGAATAA
GGAGAAAACAAAGCAAATAATAATAATAATAATAATAATTTGGGAGTTTCTATGATACCTGTTAGATTAAATAA
TTCACTACAATGACTCACAGAATTCACAAAAGTACTCTGGTTACTATCAGAGTATTATGATAAAGGGTGAACATCTTTTT
GTGCCCTTATTTATGCTTCTGGCTCATCAGTGTGTTCTCCAACAGGAAGCTCCGCCAAGTCTCAGTGTCCAGAGATT
TTGTTGGGGTTTCAATTATGTAAGGCAAATGAATACAGTCTCCAGCCCCCTCCTGTCTCCAGAGGTCATCCAGTTCTTAC
CCTGTAATCACAGAATTGGTCTTTTGGTGGCCACTTGGCATCCTGAAGCTATCCAGGGGCCAGCATGAGTCACCTCAT
TAGCATCACAAAGACACCCATCACTGAGGAAATTTAAGTGTCTTCAAGCTCTGTGCTAGGAAATGGAGACAAAGACCA
GACATATTCTTTTATATACACAGCTGATGCTGCCACTCAGCCCAACTCACATGTCCATGAATGAGCTTTCTAAGTTA
CTGGAATAGTGAAGTGAAGGTATCATTAAGGGCCCTGGGACAGAGGACCATTACCATCTAGCAAACCTATAAAATG
AAAGGTCCAAACTCCAGTTCCATCTTCCAGGATATGAAGAAGATAATGAAGAGGGGAAGAATTGGCCAAATGAAGAG
TTTGTTTTTCTACATTTTTCAGAATGCTTCTCACTTAAGACACATTCCTTAGCCTCGGCTTGAAAGCAGTGGCTGTGGT
AAGAGTTTAACTAATCTTCAGACACACATGTCTGGGAGATGGAGTTGGCCGTGTGCCACAGTGATCTGTACATAGCACA
AGCTGTGTAAATGTGACCTCCCTCAGCCAAGGTGCCCTTTTCCCTCTTTTAAATTTCCAGGGTAGGTTGTGAGAGTT
TGGAATGAGAGTCTGAACCCAGAGTTACAACCAGATTTCAATTATACTAAGTCGTGATTACAGTCTGAGGTGAGTACCC
CACTCATCCCTTTTCACTGGGTGAGTGTCCAGCATCTGAAGTCACTGTTTCTTCTAAGAGATTGTGCTCTTTTAA
TGAGTACTTATTCGCTCTGTGTTGAGGGTGGAGGTGATGTGAGTGTGTTTAAATGAGGCCTAGGCAGTAAATTCAG
TTTTGGTGTTTAGTTCTATGAGTTTGTACAAACACATGTGACTACCTTCAATAACCAAGATATAGAACAGATCCACCACTC
CAAAATACTTCCCGTGCCCATTTGGTAGTCCATGTTGCAATAGTTCCTTCCCTTCCGTGCTGAGTAGTATTCTGTTGTG
GACTACCTCACCATTTGCTTGTAAATTTCCCACTGGAGTGACATTTGGGTTGTTTCTAGTCTTTGTATGAATAAAGTTG
CTGGAGACATTTGTGTACAGGTTTTGTATGGACATAAGCTTTCAATTTCTCTCTGTACACACATAGGAGTGGGGTGTCT
GGGTCCAATGGTAGTGAGTTTAACTGCATAAGAGACCGCCAGCTTCTTCTGCAAGTAGCTGTGCATTTTGCATTCCCA
CCCTCTGTGTATGACAGCTCTAGCTGATCTCCATCCTTGCCAGCACTTGATATTGTTAGTTTTCTTTAGTTCCGGCCATT
ATGCTTCTCTATAACTGTGAGGTAGTCAATTGTCATTCTGTAAAGGAAAGTTGTCTCTTTGGAATAGCAGTTTGCAAACT
CTCATACCAAGGCTTCCACTGTGGATCAGTTTGTCTGTGCTAGGAAGGTGCGGCCGGTGGCCCTCACTCTCCCCACAGGCA
CATTTCCCTCTCCCTCTTGCAGCCCCCTTCTGTCTTGGGGTGGAGAGGAGGAAGTCTGTCTGGCCACATTTCTCCCTG
CATCTGTAGCTTTTCTGCACTGGGCAGGGCGGTGCGGCACGCGGTGTTCTGTCATGCCCCCTCCATTGCGTCAGGGATGG
CCGTTTGCAGAATAGCTCATCTTCTCCCTCCGTGCCCTTTTCCCTTAGGCCTACATACAGATCACTTTTGTGGAGCCCT
ACTTTGATGAGTATGAGATGAAAGACAGGGTCACATACTTTGAGAAGAATTTCAACCTCCGGAGGTTTATGTACACCACC
CCGTTCAACCTGGAGGGGGCGGCTCGGGGAGAGCTGCATGAGCAGTACAGAAGGAACACAGTCCCTGACCACTATGCACGC
CTTCCCTTACATCAAGACCAGGATCAGCGTCATCCAGAAGGAGGAGTAATGCACCCAAGGGATTGGCCACCCTGGATG
AGTGGGCTGGGTGGCCTCCAGGAGGACCCACAAACCTCTTTCACAGTGGATTGGACTGAAAACAGGAGGGATGCATTT

FIG. 7B (10 of 15)

GAAATATGATTATATGGTTGTCCTTTCACTCTCATAGTGCCAGAAAATCCCATTTAGGCAGCTACATATTTTATAGCACT
ATTGTATATTAATATTTAATATTTTAAAGTTATATCTTTAGTATAAGTGTGTTTATGTATTTAATTATAATATTTAATA
TATATTTCAATTATAAACTTGTACAACAGATATATTTACCTTTTAAATATTTTATATAAAATTTTCTATATTTCAAAGC
TTAGAGGTGATTCAAGCATAGTCGTGCTGTTAATTATTTGGAGACGGGACCTGCACGTGGGCAGCCCCAGTGAGCGGGTGG
TGTGCTGTGGGAAAGGGCCGTGTAAGGTAGACAAGTTCACTGACTAGCTTCTAGTCCTAGCTTCCTCCTGTGATTTTAAA
CAAGCTACGTACCTTCAGTTTCTTCATCTATGCATTAGCAGGAAAGACCTCTAAGTACAGTACAAGATTATACTCATTTT
ATTAATAAAAGGACTGGTCAAGAAGGTCTCTCAAACACAGAATTGTTTCAAATTTCTACACACCATAAAACAATTATTAT
TCTTTAAACACATATATACACTTATTTGTCGTCCTTTTATGCAGGGCCACAGACTTCTCTGTGACTGTGGGTTTGC
TGATCACAAATTCAGCATTTTCTTTTATAAACACACCCGTAGTGCTTTGTCCATGATTTTCAGTTTGTCTTTGTGTAAGC
AGAGTGAGAGCTTAAAGATCCTTGTAAACAATTTGAGAGCAGAAGCCTTCTGGATGTTTATGATGTTTTTCTCCCCGAG
ACTTTGACAGCAGTCTTGTGCACACCTAATATGACAGGAATTTTATAGCAACTCACTTTCATAATATCTTGTCCAACCA
TTTGGCTTGGTTTTTATAGAAAGAAATCTTTTCTTTCCACACCCATGGTTCATCAGTTTCTCCATTATCTAATTAGATT
GGGTCAATAAAATAACAAGTATAACAGGCATAATCAAGTTGGTGAACAAACACAGATGAATTGTGGTGAATATATACCTC
ATCAGGCAGAAAGCAGAAATAGCTGAGCTAACTGGAGAGTCACTCAGCAGGTAGTGTTTCACTGGGTAAACCATCAGGT
GTGGCTTTTACAGAAAGCTGAAGAAAGCCTGAAGCAGTGAATCAGTCAGTCGGGAGGAGGTGGGTTTGAAGCCATCTGCTGTAC
TTCCTATACTTCTTGGTTTGGACTTTTGAACACTGAGACATTCTAGGCATAACACAGATATAAACTCATGGTGGCCAAAA
GCATTTCAAACCTTTTCTTTTCTTCATTCTGCTTCTCTTTCTTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTG
TGTCTCTGCTCTCTTCTCTCTTTTCTCTCTTTTCTCTTTTCTCTCTTTTCTCTCTTTTCTCTCTTTTCTCTCTTTTCTG
TGGCTCACTGCAGCCTCGACCTCCTGGGCTCGAGCAATTTTCTACCTCAGCCTCCTGTGTAGCTGGGACTACAGGCTTG
TGCCACCTTGCCAGCTAATTAATAATACAGAGAGATATATATTTTGTAAAGAGACAGGGGTCTTACTTTGTTGGCCAGTC
TGGTCTCAAACCTGTTGGCCTCAAACGATCCTCCTACCTCAGCCTCCCAAGGTGCTGGGATTACAAGTGTGAGCCACTGCA
CCAGCCTGAAGTTTTCTTGGCCTTCTTCTGTTCCCCAACACCTCAACAACAGTCTCAGCTGTTTGTAGGGCTGTAGA
ACAAAGTCCATAGACTGGGTGGCTTAAACAACCTGAAATTTACTGTCTGCACAATTCTAGAGGCTAGAAGTTTGAATCA
AGGTGCCAGCACTGTTGGTGCCTTCTGAGGGCTGTGAGGAAAGGTCTGTTCCAGGCCTCTCTCCCTGACCTGTGGACAG
CCCTCTTCTCCCTGTGTCTCTTACATCATCTTCCCTCTGTGTTCTGTGTCAGATTTCTCTCTGTAAGGACACAGT
CATATTGCACTAGGGCTTACCCGTGCTGGCCTCATTTTAACTTGTGCTGCTCTGTAAAGACCCCTATCTCCAAAGAGGTCA
CATTCTGAGGTACTGAAGTTAGGACTTCGACATATACATTTTGGGGGAACACAATTCAACCTATAAAATTCAGAAAAGA
CTCTACCCCAAACAGCAGAACTTAGCAAAATAGATTGATTGACCTTAAAGAATTCATTTACTGGAAATTCACCCCTCA
GTTGGAGAAGGCACAGGTGATATCAAAAGCCTGTGTTATGATGGGGAGAAAATCTTGAGTGCTGTGCTTCTACTACAGC
TTTCTGCATTGTAAGTTGAGTAACATGAGGCTGTGTGCGGTGGCTCTTGCCTGTAATCCAGCACTTTGGGAGGCCGAGG
CAGGGGGATTGCCCTAAGGTTGGGAGTTTGAGACAGCCTGGCCAAACATAGAGAAACCGCATCTCTACTAAAAATACAAAA
TTATCTGGGTGTGGTGGTGCATGCCGTGTAATCCAGCTACTTGGGAGGCTGAGGCAGGAGAATTGCTTGAACCCGGGAGG
CGGAGATTGCACTGAGCCAAGATCATGCCATTGCACTCCAGCCTAGACAACAAGAGCAAACTCCATCTCAAATAAATAA
ATAAATAAATAAGTAAGTTGAGTAACCTTGCTCAGTAATAGGAAAGGCACCTGACAGGGTAGAAAAACATGGACTTTGA
AGATAGACATACTTGTGATCGAATTATGACCTCCTCCCTTACTACCTGTGGCATTCTGTGGAACCTTAACCTTACAAATCC
CCCTTTGACTGTAAAAATGGAGAGTATAAAGAGGTTGTTGAGAGGAATAAATGCTAAATGTATGTAAAGTTTCTTGAACAT
AAGGAATCAAGAAATGTTAGGCCATCTTTCTTTTAACTGTTAAGAGTATTTTAAATTACTCTGAAAGTCTTTCCCTA
GCTGCCCTCTCAAATTCAGGTGGCCTCTCTGTCTAGCTCCAGGCTTGTCCATAGCTTATGAGACCAGACAGTACTTCC
CTATGTTTACGTCTCATGTTTCTGTTTGTGACACCGATTGAAGTTGCCATTGAAGACATGAAGAAGAAGACCTGCAG
TTAGCAGTTGCCATTAACAGGAGCCGCTGATGCAAGATGCTTCAGATGGTGCTGCAAGGCTCTGTGGGAGCTACTGT
AAATCAGGTAAGCAAAACAGAGGTGGCAGCTCCTCTGGTTCTTATTATTTAGGTTGTCATTATACGTCTGCACCCCTTCT
TCCTTGGGGTTGATGAGGACTTTGATCCATAGACAAACACAGAAATGTTTCTTACACTTAACCTGAACACCTGTAAGGTTT
AGAAGACTTTTAGGAAACCTCTTCCCTTTTCTGTAACAACCCAGGTAAAAAAGAAATCTTAGAGATGAGTGGACAGGC
TTTAAGGAGTACCCTTTCTCAGAGGAGTCTCCACTTCGGGGCCAGACCTGACAATATGATGCAAACTCTGGAGTCATGTT
GAAGAATGCTTAGTCATGACCAATTCACGCAGAGTAATTGCAGGGCTTGAGACTCACCTACAAATGCCTATAGGAGAGAA
GGAAAAGGATCTAGAACATCCAACCTCTTGGCTCAGTCAGCAGATGAACCCAGCATGCCAAGGACCTTGACAACCAGGAAT
GACCTGGGACCTGACTTCTTAGGCTACTTCAGACAAGACTAGATCTTCTATCAGACTTCTTGAACCGCTGACTCCCAAG
TTCAGCATGGTGCTCAAGCAGTCTCAGATGAAGGGAGGTACCAGCCTAATACCTCTGTCCAGTGGGCTCCTTAAATCAA
ATCTAGATCTGTTCTTGTCCACACTTCCACGGCAGTTATTCAGTGAGCATCATGAGTCTTTTCTCATTTCAGCGTAATTGG
ATTTCCCCACAAAAGTTCTGAGTGTACTTGACATCAAGGGAGCAGAAACAGAGAAGAGAAATGCCTATTACATTTCCCAAG
ATCAGGAAAAAATGAGGAAACGTTTGCCTTTGTAAGTGCCAATCCTTTGATAAAATGGAAGACTTTCCAAGCCACACA
ACCATGGTCTATCTGTACACGATGGATATCTCTGACTCAATCCAGCAGTTATGCAAAATGATGTTTGGCCATGAAGGCAAC
TAGATAAGTGAACAAAAATGAATAGATCAAGGCAATCCTGATTTTTAGAAAAGCAACTCAAAGCACATACCATTGATGT
AGTTGTATTACACTTATATATGAATGAAAATCTATTATTAGTAGTATTTGATTGATAAAATAATATTCGGCGCCAGGCTC
AGTGGCTCATGCCTATAATCCCAGCACTGTGGGAGGCCGAGGTGGGTGAATCACTTGAGGTGAGGAGTTTTCAGACCAGCC
TGGCCAACATGGTGAACCCCATCTCTGCTAAAAATACAAAAATTAGCCAGTGTGGTGGCAGGCGCTGTAGTCCCAGTA
CTTGGGAGGCTGAGGCAGGAGAATCCCTTGAACCCGGGAGGTGGAGGTTGTAGTGAGCTGAGATTATGCCACTGCGCTCC

FIG. 7B (11 of 15)

TATGTGAGAACAAAAAAGCAACATGCTCAAACCTGCTGCACCTTGAACCAACTATAGACGTCAGTTCATCCATTCA
TTCAGCAGTTATTGAGCTCCTACTTTGTGCCAGGCACTGTGCTACATATGTGGAAGGATGAAGTCCCAATATCAGTAGGA
CAAGGCTACAGACAAAACAGTACTGCTGCTCATTATTCATCTCTATGTGCAAAACACAACAGATGGCCTGCCCTCCACTTC
ATTCTACAGAGATCAGAAGTCGTGGGTGAGAGTGTGCTGATGGTGCACAACTGTGTAAATTACTAAAACCTCATCAAACCTC
TAAACATAAAATGGGTGAATGTACGGTATGTAAATCATACCTGAATACAGATAGTAGATGAGGTTCTCTGTGTGCTTA
ATTGCTTCTCAAGTCCAATCTGGAAGTTACAGCTTTTAATGAATAGAGTAACTATTTTTTTCAGGTTGTTGTGCTGTGTA
TTTTCTCTCCACTCTGCTAACAGACAGCAGAGGTGACGAGAGTGGAAAAATATTTGGGGCTTGAACAGCTCTCAGGTT
TCCCCTTTAGTAAGCTCCAGCTTCTCAGCAGACTTGGGCTGTAGATCGATAAGCCCAGATTTCCAAGGTGACCATAAATG
AGTCTCTGTTGCTGAGAGCTAATAGCGGAAACATTTGCTTGCCAGGTCCACTGCGTCTAGTGCCACCACGGGGCAGCGAC
CTTTCTGACTCAGCTGTAGTGGAAGCAGAAACAGCCATAAAGAACTCTGCGCAGCTGATTTGCTGCGAGCCAGTACTCATC
CAGCCAGTCTGCAACTCTTCAAACCTGTTACCAAGCTGGGACCTCAATCAGCTTCTGTCTTTTCTGCAATAATAAAAAA
CATCTCGGGTTTCAAGCCAAAGACAAGAAGATAGAGAGATACAATCTTCTATCTTCTCTCTGCTCCCCCAACACCCC
GACCAATTTAGATTTTAAATTTTCTTCTTATACCTTATCTGAGCTTCTCATCTTATAAAGACTAAGTGATGTTAAAT
TGTTTTTAATTTAAATAAAGATAGTAGTACTACTGGCACCAGTTACAGCTTGCCCTTTAAGAGAAGTAGTTTCAGATAC
ACCCTGAAAGGGTTCTGCAGCATATATGTGGTCATAGGCTCAGAAAACAGGCTGTTGAGTGGTGGCGTTTTTAACTGGA
GTTGGGGTCTATGAAGAGGAAGGAGAAGGAATTTGTCGAGTAGCCAAAGGACAACCAATGTGTAGAGTGTAGGTGGAA
AAAGAAGCAGTAGTTTAACTTGAGACCAAGGCCATATGCCTGGCTTATAGCTGGAAATGGGGAATGGCTTTCTAGGC
AGTATATGTGGCGTTGGGGTTGGGAATATGGGCACTCAAGCCAGATTGCTGAGTTCAGATCCCATTCTGCCTCAACTAG
ATGTGTGACCCCTGAGAAGTTACCTACCCTCGGTTTCCCAGATGTAAATCGGAATAATAATTGTACCTCTCCCTTGCAG
TTAGTGACAGAATAAAATGAGTTAATACATGGAACCTTAGAATAAGACTTCATACATACTAAGGGATCAGTAAGTGAACA
TTGTTCACTGGGGCAATAGGGGACTGATGGATTTGAGTGGGAAATAGAGAATTAATCTGACTTAAATACGGAGATTGTC
TATCCATGATTTGTCTGTCTCTATAAAGTTTGAATCATAGACACAGTGATGCTGATGAGACATTGGCCTGGGAGCAGCA
GGATTTCTGGGTTTATATCCAGCTGTGCTGTCCCACAGGTATGTGACTGGACAGGGCACTTCACCTCTTGCATGTTAGTT
TCATCAACTATGAAATAAAGAGACTAGAATACAGCATCTCTAATAGTTTATCATTCTCATATTGTACAAATAGTTCATTT
ACTTAGCCTGGGTCTGTGAGGCATAATAACGCTACCATGTGCTCTGGCTTCAGCTGTGTGCAGGGACTCTTCTGAACATT
TGATATGTTTCAACTAATTTAATCTTTACATTAATTTATGAGGTAGGCTCTTATCACCCACACATCAGATGAAGAAAC
TATGACATGAAGAGGTTAAGTAGCTTGTTTAAAGGTTGCAAAGCCAGTAAGCAGCAAAGCGGGATTACAGAGTTGAGCACT
TGGCTCCAGAGTCCATCTCTTAATTGCCATGCTGAGCTGTTCCCTCTAGTGACTATATTCAGTTGCTAGTAACAGAAGG
AAGAGTAGCTTAAATAAGAAATTTATTTTTCTCTCACATTAATAAGATTGGAGGTAGTGCATGTAGAGCTGTGTAGTGG
CCTCATAAAGTCATCAGAGACCTGGTTCTTTTCCAATCCTTTGCCATGCCATCCTGGTTCTAGTGTACCCATTCTCGTG
GTCATGATATGGTTGCTAGGGCTCCAGCCATCATGACCACATCTAGGCAAGTCAGGAGTAGAAATGAGGAAACAGCAAAA
AGATGTGCCCATTTCCAGTGCCCTTACCTATATTTATCAGCGATCCCTACCTGCATGGGAGGCTAGGAAGTGTAGTTTT
CAGGTGGTCACACTGCCCTGGAGTTCTGCCAGTAGGGAAGAAAGATGGATATTGAGAAAACAATAACGAATGTTTGTCT
GCCACACTGAGGAACCCATGTATGGGCTGTGCTGAAAAGGGGGGCCAAGGCTGGGTACAGTGGCTACGCCCTGTAATCCC
AGTACTTTGGGAGGCTGAGGTGGCGGATCACTTGAGCTCACAAGTTTCGAGAGCCAGCCTGGGCAACATGGCAAAACCTCG
TCTTTACAAAAAATACAAAAAAATTAACCGGGTGTAGTGGCGTGCCTGTAGTTCCAAGTCTCGGGAAGCTGAGGTGGG
AGGATCACTTGAGCCAGGAGGAGAGGTTGCAGTGAGCTGAGATCATGCCACTGCCTTCCACCCTGCATGACAGAATGA
GATCCTCTCTCTAAAAATAGAGGGGGTACCAAGAGATGCAGGGGGGGTGAGGGCAGCATGACTACTCTCTCTGTAGGAGA
CCTTAACTCTATAAATGGAGGCCCAAAATGTTACTGCCATCAAAGCCAGGAATCCTTTTCTGGAGGCGTAACCTCCTG
CCCTTTCTAATCCCTATCAATCTGGTTTCTGTAGAAGTGTGACTGCTAGAAAACCCAGGCATATTTGTTCTAAGAAAAAT
ACTTGTGTTCCGTGAATTTACCAACAAAGGGAGCATCAGAGGATGTGAGGGAAGTCTGGAATGGTTGTATCACTAAGTGA
GAGCAGCACAGATGTTTGTGGACCTATTGAGAATGTTACAGATAAGACCATTTTGAAGAGTTGTTTGCAGTGTCAATTT
ATGATCTTGTGTACATTTTCCAAGCGATGTGGCTATTCTCTAGGAGGGATAGTAGAAATATTTCAATTTTAAATCAAATA
ACCTAGAGAATATAACCCAAATGACTGAAAGGAAGAAATGTAGAAAAAGTATATAAAATAATTTTTTGCATTATAAAAGT
TTAAAGACATAAAGTAATATTACTACATAAAATCTAAGTTTTTTACTCCAGCTATTAATATGTTTTTCTTTATAAAACAT
CACATTTATTAATGCTGTGTAAACAACTACCTCACAATTTAGTGGCTTAAAAGAAAATTTAATTATTATGCATGTGGTA
CATAATAATTTTTGCTTTTCTCTACTCTGATACTTGCCATGATGTGGTGTGATGGCTGGGGCCCTAGCGAGG
TGTATTGTGGCCATGAGAATGGTTTGTGCAACTTGGGGTGGCTGGGCTCAGCTAAGCAGTTTTTGGCTGGAGTCTCT
CAGTTGCACTGAGACAGTGACTAGGACTTGAATTACCTGAATGCTTCTCTCACTCATGTCTGGTGTCTGGGCTGAGAATAC
TCAAACAGCAGGGGCTCCTCCTCTCTAATCTCCTTCTCTCCACATGGTCTCTCCTGCATGACAGCTTTAGGGTAACCT
AGACTTGTACAGGATGGTTTCAAGACTCTTATAGTACAGAACGAGAGAGACAGAGGCCATATTACCTTTTATTAGCCA
GTCACACAGTACCACCTCCACCACATCTTATCAGTGTGGCTGTACAAAGAACCATCCACCTCTTGATGGGGGCATGGG
CAAGGTTCTAGGAGAGCACATTTCTGTGGCCATTTTCAAGAAATACAATCTGTACACTCCAGAAGCATCTGTTTGCCTTA
TTATCATAGCTTCTGATTTAATTTCTCCAGCAACCCTAGGAGATTATATGAGCTTATTATCCCCATTTTCCAGAGAAAAT
TGAAGATTTTATGGTTAAGTCATCTGCTAATGAGTAGCAGCTGTTTCAACCGCAGTTGTCTGCATATAACACATTTA
ACTCAGTCAAGGGCAGATGGTGAGCAATCAGAAGGTTGTAGCTAGCTGCTGCTACTTCTGCAAAACAAAGACTAAGGAGAG
TTTAGCTGATTTTACCAAGTTGTCCGAGTAGACTTCCCCAATTAGCTGTTAGCTTTGGCAGGACTCATCCACCTCTCT

FIG. 7B (13 of 15)

TCCGATAATGCTTTGCTTTTTTCTTATGTCACCTCTTGTGTACTATCTATTTTTCTCCTCTCTGGGACCAAGTTTCTTTT
 TATAAAGCAATAATATCTCTGTTTTTCATTTTCAGAACATTGTGCTGTCTGTCAGCATATGTATATCAGCTACAAAATATAT
 TCAACTTTGACTTCTTTTGACAAAGGACTTTAGGAAAAAGAGGAACAAAGACATTATTTGAGAATTAATATATATTTT
 TAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAAATGCAAGCTAAATGTTTCCCTTTGCAACTCATGCTT
 TGTGTTTTGTTTTGATGACCTACTCGCTCGTAATGTTTTGTAAGGCACTTCAGAGAGAAGACAGATGCATCATCTGGCC
 TCCATCAATAACACTATCCAAGGTGGCACCTCTTCTGCAATGTTTAACCTGCTAGTAATGAACGATGACTTAGTTCGG
 ATATTTTCAAGAACTTTTGTATATACCATCAGGTATGCATGAATTTATAATCTGAAAGAGGACTTAAAAATAAATAAAA
 CTTACCAGCTTAAGTGCTAACTTTTTATTTTTTAGGTATTGGGGAAGAACTCTTTTAAAGTATACACCTAACTGCTT
 TTTAAATGAGTACACATGACATACTTTAATTCATATGTATTCCCTACTCTTTGGGAGACACTGTGTTGAGACCAAGG
 TCAAAAAACGTGGTCACCGCCCTCCAAATCGTCTCCGTTCCTGAGGAAGATCATATACCTGTGTAGTAGCCACAGTACA
 AAACAGACTAGAACACAGCCCATAGCATGTAACCTTTTCTGACTAACTCAAGGATAGGCCAACACCTATGGTATTAGAT
 TCTGCCCCAAAACAATAAGAGTTAGATGCTAAGTTATATAGTCCTGGACCTTAACTCAAATAGCCAGAATAGCCCTAGTA
 ACCTAGAATATTCCTGATTAAATATCCCTGCTTTTAGATACCTGTTGTCCATTTGGGTTTGTTTTTTACAGTCTCTTTT
 GTACCACAGTGGATACATTTGCTTCATGAGTGCAGGAACCATGTTCACTGCTGCATTCTTACCCCTAGCCCTGCAACAAA
 CACACAAAAGATACCCAATAAATATTTGTTGATTCTACTAAATGAATGAATGATGAGTAGGCTGCTTCTAGAAGTGCACT
 GCCAATAAGAATGTAATGCAAGCCACATATATAATTTTAAAAATTTCTAGTAGCCATATTAAAAATAATAATAGGCCAAGT
 GCAGTGGCTCATACATGTAATACCAGCAGTTTGAAGACCAAGGTGGGCAGATCACTTGAGCCAGGAGTTTGAGACCAG
 CCTGGGCAACATGGCTAAACCCCATCTCTACCAAAAAAGATATAAAAAATTAACCAAGTGTGGTGGCATGTGCCTGTAGT
 CCCAGCTACTCGGGAGGCTAAGGTGGGAGGATCGCTTGAGCCCAGAAGGTTGAGGCTGCAGTGAGCCATGATCGTGCAC
 TGCACCTCTAGCCTGGGTGACAGAGTGAGACCCTGTCTCAAAAAATAATCAGCATCATAAAAAAGAAACCAGCAAAATTAAC
 TTTACTAGTATATTTAACCCAATATATATAAATATTTTCAATATGCTTCCACTATAAAAAATTTATTTACAGTCTTTT
 TATTTCCATATTAAGTCTTTAAAAATCTGATGTGTAGTTTGTACTTACAGCACGTTGCAGTTAGGACTGGCCACATTTTA
 AGTGCACAGTAGCCACAGGGGGCCACTGGCTACCATATTGGATAGTGCCATTCTAGAAGCTTTCAGCTTTTCAACTGGA
 TGCCTCTGATTTGTGGACTCAGAATACAGATAACCAAAGAAGTGGGACTAGTGTCTGAAGTAAGAATGACAGGGTATGAT
 TGAGAGCCCCATGAGCTTACCTAGGAGAGAACTTGTGGGTTGCAGAATAAGGATTTGTCAATATTGGCTCTAGCTGTT
 CACACTATTTCTGGGCAACTCCAGATCATTTCTCACTCCAGATAGTTAAGTGGGGAGCATGGCTGCACTTTTTTAAAG
 TGATGGCACAACAAAAGATATTGAACGTTGGTCTCTGATTATATATTCTAAATATGCAGTTAGAAAAGAGGCCTTTTAA
 GAATCCCTAAGAGTAAAGCAAATTAGTATCTTTGTTTCTGAAAATTAGAGAACTTGATATGCCATGATAGCCCTCTTC
 ATTTTATTTGGAAAACCTCTTCTATGAAAGCTTATTAGAGAAAATTTCTGATTAGCTTCATGCCTCCCTCTCTTCAGCAA
 GGTCAAGGGTGCAGTTGTCATATCACATAAGAATCTCATAAAAAATTAACATGAATATACTGCACAGATCTGATTGGGT
 TTGTCTATGCCACACATTGTTTTAAATTCCTAATTCTATTCTATAAAGAGTGTTTCTATGACAATAGATCGTTTTTAAAA
 ACAACAAAACAAAATTTAGAGTTGTCATTGGTAATTGTGGTTGCAAGTATGCTTTCAAAGACCAGAAGCTTTTGT
 TTGCTTTGAATGTAATTTTTTCTTTTTTCTTTTTGATACGGAGTCTCACTCTGTTGCCAGGCTGGAGTGCATTGGCAC
 CATCTCAGCTCACTGCAACCTCCACCTCCGTGGTTCAAGCAATTCCTGCTCAGCTCCTGAGTAGCTGGGATTACAG
 GCGTCCACCACCAGCTGACTAATTTTTGTATTTTGTAGAGATGGGGTTTTACCATGTTGGCCAAGCTGGTCTCAAA
 TTCTTGACCTCAGGTGATCCACCTGCCTCTGCCTCCCAAAGTGCTG

FIG. 7B (15 of 15)

GGAACAATTTCTCTCATGTGTATGGCTCCCTAAAGTGTGGCTGAGCATTGTCCACATGGGTG
 ATGCAAAGGATCACTGAACTAGGAGCAGTTGGGAAAAATACAATCATTGGGAATTCCTGTAGC
 ATCGAATGTGCTACAGGGAGGTAGAAGTATTCATACAACAGTTCTCTGGTGTTCCTGTGTGTA
 GCAACCAGTCAGCCAAAAGGGTTCAGCTGCTTGAATGAGAATGGCTGGATCAAAATGGCAGCT
 CATGATTTAAAGGATTCTAGTCAGATACCAGACATCCTCACATAGAGAAAACCTGAATGGCTG
 GGGGAGAAGGAGTCAAATGCCCTGGATCTTTTCTTGGGCCTCAAAGTCTCTCTGTGCATCA
 TCCTTCCAGTATTGGGCAGGACCTGACTGCAGGCATCATGGCCTCTGTGAACCTCTCAAGGGTA
 TGTATTATCTGACAAAACCTACGATGTCCACTAACAGGCCACTGAAAGGTATCTTAGTCAGTTC
 TGCTCATTGCCAGCCAAGGCCTACGTTTTATAACATGATATCAAAGATTGCATCTAAAATTGT
 GATGATTTCCATAAATAATCATTTTATTTAGATTTTTCTATTTTAAATCCAAGGTATCTTCAGC
 GGAAATAAGGAAACAGTTTACTCTCCACCAAACCTTGGCCAGTACCATCGACAGAGCATAAGT
 ACCTCTGGCTTCCCTCTCTTCACTAGTAAGTATGAGTTCAGGTTTACTTAGCGATTGGTCA
 AGTGCAAAAGTGCCAGGGTATGTGTTGCCTCCTGTTCCCTTAGATCTTCTACCATCACCTCA
 CATTCTCCAGTCACCAGATCCTAATCTGTGACTGTGTCTGGACATCAGACAATATCCCTCTCT
 CTCTCTGCCAACCGGTACTTAGGGTACATAATAGAACCCTGGGAGCTGTGGTTTTGATGTCTC
 TAGACTAGGTGGGCTTCCAGGTGACTCAGTCTCATCCAATTATGGTTCATATTTGGGGGAGAA
 GGGCTAGCCCAAAAACCTACCACCATTGTAGTATGCATTTTTTTGGAAAAGCATATTCAAAA
 TCTGAAATGCCAAGTTACAGACCTCCTTTTTGTAAAATAATTTCTTGCTAGTATAATTTACAT
 ATAATAAAATTCACACATTTTAGGTGTACAATTTGGTGAACCTGGGCAACTTAGAGTCACTTAA
 CCTTTCCTCAGTCAAGATATAGAACCTTCTTTTATCCTAAAGCGTTCCCCAGCGCGCTTTTAC
 AATCTCCTCTCCCCAGGCCACACCTCCAACCTCACGCAATCTCTGACTCACTTCTGTCAACATA
 ATTTTGCTCTATCTGGAGCTTCATATCCTGTTACAGTATGTACAAACCTTCTTTTTTTGAGACA
 GGGTGTCTAGTCTGTCAACCAGCCTGGAGTACAGAGGTGTGATCTCAGCTCACTGCAACCTCAAC
 CTCCCAGGATCAGATGATCTCCTCCACCTCATCCTCCCAAGTAGCCGGGACTACAGGCGCAT
 GCCACCACACCTGGCTAATTTTTGTACTTTTTGTAGAGACAGGGGTCTCGCTATGTTGCCAGG
 CTGGTCTTGAACCTCTGGGCTCAAGCGATCCTCCTGCCTCAGCCTCCCAAAGTGTGGGATTAC
 AGTGAGCCACTGCACCTGGCCCTAAACCTTCATTTTTTAAACACATTTCTCTTAAATTGAAGA
 TTGCCTACATTTTTATATCAATGCCAATTGTTGAGTGTGCCTATATGTGTTATATTTGAGC
 ACTAAATGCCAGATGTGTGCCAAGTGAGATAAATCTGACAAATGAGATGGTTTTGTAAACCAGC
 AGTGAATATTCACCTCCTGTGTGAGAGAGCTCCAGCCCTCCTGTACTCACTTCTCTCACACAGCA
 CAGCAGCACTCTTGCTGGTCTGTGCTGCTTATCTTGAAGAGGTTAGGTTACTTTTTGTTTCTACT
 TATTACTTCGAAACCACTTCTGCCTTAGAAATTTGTAACTTCCGCTCAGTTTTCCGGTAACCG
CCATTTTGTCTCCTGTAACAATTTACGCGCGTGTAACCTGTGAATCTTT

FIG. 7C

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hCLASP4 -----MFPMEDISISVIGRQRRTVQ----- 20
hCLASP5 -----MTHLNSLDVQLAQELG----- 16
hCLASP3 -----MAERRAFAQKISRTVAAEVRKQISGQYSGSPQLLKNLNIVG 41
hCLASP2 -----MLLFYDDFQTAILRRQGRYICS----- 23
hCLASP7 -----MAASERRAFAHKINRTVAAEVRKQVSRERSGSPHSSRRCSSSL 43
hCLASP1 MSFRGKVFVKREPSEFWKKRRTVRRVIQEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN 60
      . . .

hCLASP4 -----STVPEDA EKRAQSLFVKECIKTYSTDWHVNYK 53
hCLASP5 -----DFT 19
hCLASP3 N-----ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP 83
hCLASP2 -----TVPAKAE EEAQSLFVTECIKTYNSDWHLVNYK 55
hCLASP7 G-----VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP 79
hCLASP1 DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDA EHKAE NLLVKEACKFYSSQWHVNYK 120
      . . .

hCLASP4 YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG 105
hCLASP5 DDDLDVVFTPKECRTLP-SLPEEGVELDPHVR-----DCVQTYIREWLI 63
hCLASP3 PDDIEVVYSRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI 126
hCLASP2 YEDYSGEFRQLPNKVVKLDKLPVHVYEVDDEVDKDED-----AASLGSKGGITKHG 107
hCLASP7 ADDLELLLPRECRTTEP-GIPKD-EKLDQVR-----AAVEMYIEDWVI 122
hCLASP1 YEQYSGDIRQLPRAEYKPEKLPSSHFEIDHEDADKDEDTSHSSSKGGGGAGGTGVFKSG 180
      . . . : * . . : * .

hCLASP4 WLHKANVNSTIT--VTMKVFKRIFYLTQLPDGSIYILNSYKDEKNSKESK-GCIYLDACI 162
hCLASP5 VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAQA--GPRHLNVLC 118
hCLASP3 VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGNSYQDDQDDLKRSMMSI 183
hCLASP2 WLYKGNMNSAIS--VTMRSFKRFFHQLIQLGDGSYNLNFKYDEKISKEPK-GSIFLDSCM 164
hCLASP7 VHRRYQYLSAAY--SPVTTDTQREKQKG-LPRQVFEQDASGDERSGPEDSNDSSRRSGSP 179
hCLASP1 WLYKGNFNSTVNNTVTVRSFKRIFYLTQLPDNSYIMNFKYDEKISKEPK-GCIFLDSC 239
      . . . : . . . * : . . . : . . .

hCLASP4 DVVQCPKMRRHAFELKMLDKYSHYLAAETE QEME EWLITLKKIIQINTDSLVEKKETVE 222
hCLASP5 DVSGKGPVTACDFDLRLSLQPDKRLNLLQQVSAEDFEKQNEEARRTN-----RQAE 169
hCLASP3 DDTPRGSWACSI FDLKNSLPDALLPNLLDRTPNEEIDRQNDQQRKSN-----RHKE 234
hCLASP2 GVVQNKNVRRFAFELKMQDKSSYLLAADSEVEME E WITL N K I L Q L N -----FEAMQEK 219
hCLASP7 EDTPRSSGASSIFDLRNLAADSLPSLLERAAPEDVDRRNETLRRQH-----RPPA 230
hCLASP1 GVVQNRLRLRYAFELKMNLDLTYFVLAATESDMDEWIHTLNRILQISPEGPLQGRSTEL 299
      * : * : . : . :

hCLASP4 TAQDDTSS----QGKAENIMASLERSMHPMLKYGRETEQLNKL SRGDGRQNLFSFDSE 278
hCLASP5 LFALYPSVD----EEDAVEIRPVPECPKEHLG-----N-----RILVKLLTLKFEIE 212
hCLASP3 LFALHPSPD----EEEP IERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE 277
hCLASP2 RNGDSHEDD----EQSKLEGSGSGLD SYLPELAKSAREAEIK---LKSESRVKLFYLDPD 272
hCLASP7 LLTLYPAPD----EDEAVERCSRPEPPREHFG-----QRLLVKCLSLKFEIE 273
hCLASP1 TDLGLDSLNSVTCECTPEETDSSENNLHADFAKYLTETEDTVKTTNRMERLNLFSLDPD 359
      . : . : : : :

hCLASP4 VQR LDFS----GIEPDIKP-FEEKCNKRFLVNCHDLTFN ILGQIGDNAKGPPTNVEPFFI 333
hCLASP5 IEPLFAS----IALYDVKERKKISENFHCDLNSDQFKGFLRAHTPSVAASSQARS AVFSV 268
hCLASP3 IEPIFAS----LALYDVKEKKKISENFYFDLNS EQMKGLLRPHVP PAAITTLARS AIFSI 333
hCLASP2 AQK LDFS----SAEPEVKS-FEEKFGK RILVKNDLSFNLOCCVAENE EGPTTNVEPFFV 327
hCLASP7 IEPIFGI----LALYDVREKKKISENFYFDLNSDSMKGLLRAGHGT HPAISTLARS AIFSV 329
hCLASP1 IDTLKLQKKDLLEPESVIKPFEEKAAKRIMICKALNSNLQGCVTENENDPITNIEPFFV 419
      . : . : . : . : . : * :

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FIG. 8 (1 of 6)

hCLASP4	NLALFDVKNCKISADFHVDLNPSPVREMLWGSSTQLASDGSP---KGSSPESYIHGIAE	390
hCLASP5	TYPSSDIYLVVKIEKVLQQGD----IGDCAEPYTVIKESDG-----GKSKE-KIEKLKL	317
hCLASP3	TYPSQDVFLVIKLEKVLQQGD----IGECAEPYMIFKEADA-----TKNKE-KLEKLKS	382
hCLASP2	TLSLFDIKYNRKISADFHVDLNFHFSVRQMLATTSPALMNGS-----GQSPSVLKGILHE	381
hCLASP7	TYPSPDIFLVIKLEKVLQQGD----ISECCEPYMVLKEVDT-----AKNKE-KLEKLRL	378
hCLASP1	SVALYDLRDSRKISADFHVDLNFHAAVRQMLLGASVALENGNIDTITPRQSEEPHIKGLPE	479
	. . * : * : . : . : : . . . :	
hCLASP4	SQLRYIQQGIFSVTNPHPEIFLVARIEKVLQGNITHCAEPIYKNSDPVKTAQKVHRTAKQ	450
hCLASP5	QAESFCQR-----LGKYRMPFAWAPISLSFFNVSTLREVTDVDVSVVGRSPVGERTLA	372
hCLASP3	QADQFCQR-----LGKYRMPFAWTAIHLMNIVSSAGSLERDSTEVEISTGERKGSWSERR	437
hCLASP2	AAMQYPKQGFISVTCPPHDI FLVARIEKVLQGSITHCAEPMKSSDSSKVAQVLKNAKQ	441
hCLASP7	AAEQFCTR-----LGRYRMPFAWTAVHLANIVSSAGQLDRDSD----SEGERRPAWTDRR	429
hCLASP1	EWLKFPKQAVFSVSNPHSEIVLVAKIEKVLGMGNIASGAEPYIKNPDNSNKYAQKILKSNRQ	539
	: : : : : :	
hCLASP4	VCSRLGQYRMPFAWAARPIFKDTQGSLLDGRFSPLYKQDSSKLSSSEDILKLLSEYKKPE	510
hCLASP5	QSRRLSERALSLEENGVS NFKTS-----TLSSVSSFFKQEGDRLSDEDLFKFLADYKRSS	427
hCLASP3	NSSIVGRSLERTTSGDDACNLTSFR-PATLTVTNFFKQEGDRLSDEDLFKFLADMRRPS	496
hCLASP2	ACQRLGQYRMPFAWAARTLFKDASGNLDKNARFSAIYRQDSNKLSDNDMLKLLADFRKPE	501
hCLASP7	---RRGPQ--DRASSGDDACSFSGFR-PATLTVTNFFKQEAERLSDEDLFKFLADMRRPS	483
hCLASP1	FCSKLKGYRRAFAWAVRSVFKDNQGNVDRDSRFSPLFRQESSKISTEDLVKLVS DYRRAD	599
	. . : : * : : * : * : * : : : : .	
hCLASP4	--KTKLQIIPGQLNITVECVPVDSLNCITSSYVPLKPFE-KNCQNITVEVEEFVPEMTKY	567
hCLASP5	SLQRRVKSIPGLLRLEISTAPEIINCCLTPEMLPVKPF--ENRTRPHKEILEFP--TREV	484
hCLASP3	SVLRLRLPITAQLKIDISPAPENPHYCLTPELLQVKLYP-DSRVREPTREILEFP--ARDV	553
hCLASP2	K-MAKLPVILGNLDITIDNVSSDFPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKH	560
hCLASP7	SLRLRLRPVTAQLKIDISPAPENPHFCLSPPELLHIKYP-PDPRGRPTKEILEFP--AREV	540
hCLASP1	R-ISKMQTIPGSLDIAVDNVPLEHPNCVTSSFI PVKPFNMMAQTEPTVEVEEFVYDSTKY	658
	: : . * : . . . : . . : * : * : * : *	
hCLASP4	CYFETIYKNHLYVYPLQLKYDSQKTFAKARNIAVCVEFRDSDSDASALKCIYKGFAGSV	627
hCLASP5	YVPHTVYRNLLYVYQRLNFVN--KLASARNITIKIQFMCG-EDASNAMPVIFGKSSGPE	541
hCLASP3	YVPNTTYRNLLYIYPQSLNFAN--RQGSARNITVKVQFMYG-EDPSNAMPVIFGKSSCSE	610
hCLASP2	TQPYTIYTNHLYVYPKYLKYDSQKSF AKARNIAICIEFKDSDEEDSQPLKCIYGRGGPV	620
hCLASP7	YAPHTSYRNLLYVYPHSLNFSS--RQGSVRNLAVRVQYMTG-EDPSQALPVIFGKSSCSE	597
hCLASP1	CRPYRVYKNQIYIYPKHLKYDSQKCFNKARNITVCIEFKNSDEESAKPLKCIYKGFEGPL	718
	* * * : : * * : : . . * : : : : . * . : : : * : * .	
hCLASP4	FTTNAYAVVSHHNQNPFEFYDEIKIELPIHLHQKHHLLFTFYHVSCEINTKGTTKKQDTVE	687
hCLASP5	FLQEVYTA VTYHNKSPDFYEEVKIKLPKLT VNHLLFTFYHISCQ-----KQGASVE	595
hCLASP3	FSKEAYTAVVYHNRS PDFHEEIKVKLPATLTDHLLFTFYHVSQ-----KQNTPLE	664
hCLASP2	FTRSAFAAVLHHHQNPEFYDEIKIELPTQLHEKHHLLFTFFHVSCDNSSKGSTKKRDRVVE	680
hCLASP7	FTREAFTPVVYHNKSPFEFYEEFKLHPACVTENHLLFTFYHVSQ-----RPGTALE	651
hCLASP1	FTSAAYTAVLHHSQNPDFSDEVKIELPTQLHEKHHILFSFYHVTCDINAKANAKKKEALE	778
	* : : * : * : * : * : * : * : : : : : : : : : : : : : *	
hCLASP4	TPVGFAWVPLLKDGRIITFEQQLPVSANLP PGYLNLDAESRRQCNVDIKWVDGAKPLLK	747
hCLASP5	TLLGYSWLPILLNERLQTGSYCLPVALEKLPPNYSMHS AEKVPLQNPPIKWAEGHKGVFN	655
hCLASP3	TPVGYTWIPMLQNGRLKTGQFCLPVSLKPPQAYSVLSPEVP---LPGMKWVDNHKG VFN	721
hCLASP2	TQVGYSWLPPLLKDG RVVTSEQHIPVSANLP SGHLGYQELGMGRHYGPEIKWVDGGKPLLK	740
hCLASP7	TPVGFTWIPLLQHGRRLTGPFCLPVSDQPPPSYSVLT PDVA---LPGMRWVDGHKG VFS	708
hCLASP1	TSVGYAWLP LMKHDQIASQEYNIPIATSLPPNYLSFQDSASGKHGGS DIKWVDGGKPLFK	838
	* : : * : * : : . : : : : * : . . . : : * : : .	

FIG. 8 (2 of 6)

hCLASP4	FKSHLESTIYTQDLHVHKFFHHCQLIQS-----GSKEVPGELIKYLKCLHAM	794
hCLASP5	IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS	715
hCLASP3	VEVAVASSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLENELKSSISALNSS	780
hCLASP2	ISTHLVSTVYTQDQHLHNFQYQCQKTES-----GAQALGNELVKYLKSLHAM	787
hCLASP7	VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLSEGNVEQELRASLAALRLA	767
hCLASP1	VSTFVVSTVNTQDPHVNAFFQECQKREKQ-----MSQSPTSINFIRSCKNLLNVE	887
	.. * : . * * : . * * : : . *	
hCLASP4	ETQVMIQFLPVLMLQLFR-----VLTNMTH-----EDDVP	824
hCLASP5	RIEPLVLFLHLVLDKLFQLSVQPMVIAGQTANFSQAFESVVAIANSNLHNSKDLQSKDHG	775
hCLASP3	QIEPVVRFLHLLLDKLI LLVIRPPVIAGQIVNLGQASFEAMASIINRLHKNLEGNHDQHG	840
hCLASP2	EGHVMI AFLPTILNQLFR-----VLT-RAT-----QEEVA	816
hCLASP7	SHEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGAFEAMHVSVLVHRSLEAAQDARG	827
hCLASP1	KIHAIMSFLPIILNQLFK-----VLVQNE-----EDEIT	916
	. : * : * : *	
hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----YLRSEFIKYS-----FRPEKP	860
hCLASP5	RNCLLASVHYVFERLPEVQRDVPKSGAPTALLDPRSHTYGRTSAAAVSSKLLQARVMSS	835
hCLASP3	RNSLLASYIHYVFRLPNTYPNSSSPG-PGGLGGSVHYATMARSAVRPASLNLNRSRSLN	899
hCLASP2	VNVTRV-IIHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY	852
hCLASP7	HCPQLAAYVHYAFRLPGTEPSLPDGAPP----VTVQAATLARGSGRPASLYLARSKSISS	883
hCLASP1	TTVTRV-LPDIIVAKCHEEQLDH-----SVQSYIKFV-----FKTRAC	952
	. . . : :	
hCLASP4	SAPQAQLIH-----ETLATTMIALKQS-----	883
hCLASP5	SNPDLAGTHSAADEEVKNIMSSKIADRNCRMSYCYSGSSDAPSSPA-----	882
hCLASP3	SNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAESTQAMDRSC	959
hCLASP2	VASEYKTVH-----EELTKSMTTILKPS-----	875
hCLASP7	SNPDLA VAPGSVDDEVSRILASKLLHEELA-LQ-----	915
hCLASP1	KE---RPVH-----EDLAKNVTGLLKS-----	972
	: . .	
hCLASP4	-----ADFLSINKLLKYS-----WFFFEIIAKSM	907
hCLASP5	-----APRPASKKHFEELALQ-----MVVSTGMVKSM	910
hCLASP3	NRMSSHTETSSFLQTLTGRLPTKKLFHEELALQWVCSGVSRESALQQA WFFFEIIMVKSM	1019
hCLASP2	-----ADFLTSNKLLRYS-----WFFFDVLIKSM	899
hCLASP7	-----WVWSSSAVREAILQHA-----WFFFQLMVKSM	942
hCLASP1	-----DSPTVKHVLKHS-----WFFFAIILKSM	995
	. * . . : ***	
Cadherin Cleavage		
hCLASP4	ATYLLLEENKIKLFRGQRFPEYHHVHLHSLLLAIIPHVTIRYAEIPDE---SRNVNYSLAS	964
hCLASP5	AQHVNMDKRDSEFRTRFSDRFMDDDITIVNVVTSEIAALLVKPQKENEQA EKMNISLAF	970
hCLASP3	VHHLYFNDKLEAEFRKSRFFPERFMDDIAALVSTIASDIVSRFQKDTM-----VERLNTSLAF	1076
hCLASP2	AQHLENSKVKLLRNQRFPA SYHHAETVNNMLPHITQKFGDNPEA---SKNANHS LAF	956
hCLASP7	ALHLLLGQRLDTRKLRFPGRFLDDITALVGSVGLVITRVHKDVEL---AEHLNASLAF	999
hCLASP1	AQHLIDTNKIQLRFPQRFPE SYQNELDNLMVVLSDHVIWKYKDALEE---TRRATHSVAR	1052
	. : . : . * ** . : . : : * : *	
hCLASP4	FLKRCLTLMDRGFIFNLINDYISGFSPKDP----KVLAEYKFEFLQTCNHEHYIPLNL	1019
hCLASP5	FLYDLLSLMDRGFVENLIRHYCSQLSAKLSNL---PTLISMRLEFLRLILCSHEHYIPLNL	1027
hCLASP3	FLNDLLSVMDRGFVESLIKSCYKQVSSKLYSLPNPSVLVSLRLDFLRLICSHEHYIPLNL	1136
hCLASP2	FIKRCFTFMDRGFVEKQINNYISCFAPGDP----KTLFEYKFEFLRVVCNHEHYIPLNL	1011
hCLASP7	FLSLLSLVDRGFVESLVRAYHKQVATRLQSSPNPAALLTLRMEFTRILCSHEHYIPLNL	1059
hCLASP1	FLKRCFTFMDRGCFVKMNNYISMFSGDL----KTLQCYKFDFLQEVQCHEHFIPCL	1107
	* : . : . * * * * * * : * : * : * : * : *	

FIG. 8 (3 of 6)

Cadherin EC motif

hCLASP4 PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGLLRETSI 1060

hCLASP5 FFMNADTAPTSP--CPSISSQNSSSCSSFQDQKIASMFDLTSEYRQQHFLTGLFTELA 1085

hCLASP3 PCSLLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELSVFPFRQQHYLAGIVLTE 1196

hCLASP2 PMPFGKGRIQR-----YQDL--QLDYSLTDEFCRNHFLVGLLREVT 1052

hCLASP7 PCCPLSPPASPSPSVSSTTSQSSTFSSQAPDPKVTSMFELSGPFRQQHFLAGILLTE 1119

hCLASP1 PIRSANIPDPLTP-----SES-----TQELHASDMPEYSVTNEFCRKHFLIGILLRE 1157

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hCLASP4 ALQDN----YEIRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQLYLPFVGLLENIQRL 1116

hCLASP5 ALDAEGEGISKVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAALYLPVGIILDALP-- 1143

hCLASP3 ILDPDAEGLFGLHKKVINMVHNLSSHSDSPRYSDFQIKARVAMLYPLIGIIMETV-- 1254

hCLASP2 ALQEFR---EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPFLGLLIENVQRI 1108

hCLASP7 ALEPEAEGAFILHKKAISAVHSLLCGHDTDPRYAEATVKARVAELYPLLSIARDTLP-- 1177

hCLASP1 ALQEDQ---DVRHLALAVLKNLMAKHSFDDRYREPRKQAIASLYMPLYGMLLDNMPRI 1213

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hCLASP4 AGRDTLYSCA-----AMPN-S---ASRDEFFPCGFTSPANRGSSTDKDTAYGS 1160

hCLASP5 -----QL-----CDFTVADTRRYRTSGSD----- 1162

hCLASP3 -----QLY-----DFTETHNQGRGPCIATDD-- 1276

hCLASP2 NVRDVSPFPVNGAMTVKDESALPA-VNPLVTPQKGSTLDNSLHKDLGAIISGIASPYTT 1167

hCLASP7 -----RLH-----DFAEGPGQSRSLASMLDSDTE 1201

hCLASP1 YLKDLYPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTSFSKDVLSIAAFSSIAIS 1273

. :

hCLASP4 FQ-NGHGIKREDSRGS LIPEGATGFPDQGNTGEN-----TRQSSSTRSSVSQYNRLDQYE 1213

hCLASP5 -----EEQEGAGAINQNVALAIAGNNFNLT-----SGIVLSSLPYKQYNMLNADT 1208

hCLASP3 -----YESESGSMISQTVAMAIAGTSVPQLTR---PGSFLLTSTSGRQHTTSAES 1324

hCLASP2 STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSSVVRCDKLDQSE 1227

hCLASP7 -----GEGDIAGTINPSVAMAIAGGPLAPGSR---ASISQGPPTASRAGCALSAES 1249

hCLASP1 -----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDRLDQAE 1327

. : . : . : . :

hCLASP4 TRSLLMCYLYIVKMISEDTLLTYWNKVSPQELINILILEVCLFHFYRMGKRNIARVHDA 1273

hCLASP5 TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYKKGKQSSDKVSTQ 1268

hCLASP3 SRSLICLLWVLKNADETVLQKWFTDLVSVLQLNRLDLLYLCVSCFEYKKGKVFERNNSL 1384

hCLASP2 IKSLLMCFLYILKSMSDDALFTYWNKASTSELMDEFTISEVCLHQFYMGKRYIARNQEG 1287

hCLASP7 SRTLLACVLWVLKNTEPALLQRWATDLTLPQLGRLLDLLYLCLAAFEYKKGKKAERINSL 1309

hCLASP1 TRSLLMCFLHIMKTISYETLIAYWQAPSPPEVSDFFSILDVCLQNFYRLGKRNIIRKIAA 1387

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hCLASP4 WLSKHFGIDR-----KSQTMPALRNRSQVMQARLQHLSSLESS----- 1311

hCLASP5 VLQKSRDVKAR-----LEEALLRGEARGEMMRRAPGNDRFPGLNEN--- 1311

hCLASP3 TFKKSKDMRAK-----LEEAILGSIGARQEMVRRSRGQLERSPSGSAFGSQ 1430

hCLASP2 LGPIVHDRKS-----QTLPVSRNRTGMMHARLQQLGSLDNS----- 1323

hCLASP7 TFKKSLDMKAR-----LEEAILGTIGARQEMVRRSRERSPFGNPEN---- 1350

hCLASP1 AFKFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHKQHRSTLPIIRGKN----- 1442

. : : :

hCLASP4 -----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFITQCFKTQLL 1359

hCLASP5 --LRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAHLIILDMQENIIQASS-ALD 1368

hCLASP3 ENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEANLIILDTLEIVQTVS-VTE 1489

hCLASP2 -----LTFNHSYGHSDADVHLQSLLEANIATEVCLTALDTLSLETLAFKNQLL 1371

hCLASP7 --VRWRKSVTHWKQTSRDRVDTKDEMEHEALVEGNLATEASLVVLDLTLEIIVQTVM-LSE 1407

hCLASP1 --ALSNPKLLQMLDNTMTSNSNEIDIVVHVDTEANIATEGCLTILDVLSLTQTHQRQLQ 1500

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FIG. 8 (4 of 6)

hCLASP4 NNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFISKFPSAFFKGRVNMCACFCY 1419
hCLASP5 CKDS---LLGGVLRVLVNSLNCDSQSTTYLTHCFATLRALIAKFGDLLFEEVEQCFLDCH 1425
hCLASP3 SKES---ILGGVLKVLHSMACNSAVYLQHC FATQALVSKFPPELLFEEETEQCADLCL 1546
hCLASP2 ADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRADMCAALCY 1431
hCLASP7 ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQALVSKFPPELLFEEDTELCADLCL 1464
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVQNSATALKHVFASLRLFVCKFPSAFFQGPADLCGSFCY 1560
. : : : * * * : : * : : * : : * : *

hCLASP4 EVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTHLQIIIAVSQLIADVALSGG 1479
hCLASP5 QVLHHCSSSMDVTRSQCACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483
hCLASP3 RLLRHCSSTIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSLSSLVGTSQNFNE 1604
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQLIADVVGIGE 1491
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSLVGTTQNFSE 1522
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSQLIADAG-IGG 1619
.: * : : * : : * : : * : : * : : *

hCLASP4 SRFQESLFIINNFANSRPMKATAFPAEVKDLTKRIRTVLMATAQMKEHEKDPPEMLIDLQ 1539
hCLASP5 EHLRRSLRTILAYSEEDTAMQMPFPPTQVEELLCNLNSILYDTVKMREFQEDPEMLMDLM 1543
hCLASP3 EFLRRSLKTILTYAEDLELRETTFPDQVQDLVFNLMILSDTVKMKEHQEDPEMLIDL 1664
hCLASP2 TRFQQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHENDPEMLVDLQ 1551
hCLASP7 EHLRRSLKTILTYAEDMGLRSTFAEQVQDLMFNLMILTDTVKMKEHQEDPEMLIDL 1582
hCLASP1 SRFQHS LAITNNFANGDKQMKNSNFAEVKDLTKRIRTVLMATAQMKEHEKDPPEMLVDLQ 1679
: : * : : * : : * : : * : : * : : *

transmembrane
hCLASP4 YSLAKSYASTPELRKTWLD SMAKIHVKNGLDSEAMCYVHVAALVAEFLHRKK----- 1592
hCLASP5 YRIAKSYQASPDRLRLTWLQNM AEKHTKKKCYTEAMCLVHAAALVAEYI SMLEDH----- 1598
hCLASP3 YRIAKGYQTSPE-RLTWLQNMAGKHSERNHAEAAQCLVHSAALVAEYI SMLEDR----- 1718
hCLASP2 YSLAKSYASTPELRKTWLD SMARIHVKNGLDSEAMCYVHVTALVAEYI TRKG----- 1604
hCLASP7 YRIARGYQGSPDLRLTWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYI ALLEDQ----- 1637
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGDLSEAMCYIHIAALIAEYI KRKG YWKVEKI 1739
* : . * : : * : : * : : * : : * : : *

hCLASP4 -----LFPNGCSAFKKITPNIDE EGAMKEDAGMMD----- 1622
hCLASP5 -----SYLPVGSVSFQNISSNVLEESVVS EDTLSPDE DGV 1633
hCLASP3 -----KYLPGCVTFQNISSNVLEESAVSDDV VSPDEEGI 1753
hCLASP2 -----VFRQGCTAFRVITPNIDE EASMMEDVGMQD----- 1634
hCLASP7 -----RHLPVGCVSFQNISSNVLEESAISD DILSPDEEGF 1672
hCLASP1 CTASLLSEDTHPCDNSNLLTTPSGGSMFSGWPAFLSITPNIKEEGA AKEDSGMHD----- 1795
: * : * : : * : : * : *

ITAM
hCLASP4 ---VHYSEEV LLELLEQCVDGLWKAERYEIISEISK LIVPIYEKRREFEKLTVYRTIHG 1679
hCLASP5 CAGQYFTESGLVGLLEQA AELFSTGGLYETVNEVYKLVIPILEAHREFRKLTLTHSKLQR 1693
hCLASP3 CSGKYFTESGLVGLLEQA AASFMSMAGMYEAVNEVYKVLIP IHEANRDAKKLSTIHGKIQE 1813
hCLASP2 ---VHFNE DVLME LLEQCADGLWKAERYELIADIYKLIPIYEKRR----- 1677
hCLASP7 CSGKHFTELGLVGLLEQAAGYFTMGGLYEAVNEVYKNLIPILEAHRDYKKLA AVHGKIQE 1732
hCLASP1 ---TPYNENILVEQLYMCGEFLWK SERYELIADV NKP IIAVFEKQ RDFKKLS DLYYDIHR 1852
: . * : : * : : * : : * : : *

ITAM DOCK motif DOCK motif ITAM
hCLASP4 AYTKLLEVMHTKKRL LGTFFRVAFYQG SFEEEDGKEYIYKEPKLTGLSEISRLVLKLYG 1739
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGF FG-SKFGDLDEQEFVYKEPAITKLP EISHRLEA FYG 1750
hCLASP3 AFSKIVHQSTGWERMFGTYFRVGF FG-TKFGDLDEQEFVYKEPAITKLA EISHRLEGFY 1872
hCLASP2 ---DFEDEDGKEYIYKEPKLTPLSEISQRLLKLYS 1710
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGF FG-AHFGDLDEQEFVYKEPSITKLA EISHRLEEFYT 1791
hCLASP1 SYLKVAE VVNSEKRLFG RYYRVAFYQG GFEEEDGKEYIYKEPKLTGLSEISQRLLKLYA 1912
* : : : : * : : * : : *

FIG. 8 (5 of 6)

	ITAM	ITAM	
hCLASP4	EKEFGTENVKIIQDS	DKVNAKELDPK	YAHIQVITVVKHYFDDKELTERKTEFERNNHNISRFV 1799
hCLASP5	QCFGAEFVEVIK	STPVDKTKLDPN	KAYIQITFVEHYFDEYEMKDRVITYFEKNFNLRRFM 1810
hCLASP3	ERFGEDVVEVIK	SNPVDKCKLDPN	KAYIQITFVEHYFDTYEMKDRITYFDKNYNLRRFM 1932
hCLASP2	DKFGSENVKMIQ	DSGKVNPKDLDS	KYAYIQVTHVIEFFDEKELQERKTEFERSHNIRRFM 1770
hCLASP7	ERFGDDVVEIIK	DSYPVDKSKLDS	KAYIQITFVEHYFDTYELKDRVITYFDRNYGLRTFL 1851
hCLASP1	DKFGADNVKIIQ	DSNVKNPKDLDP	KYAYIQVTHVTFEFEKEIEDRKTDFEMHHNINRFV 1972
	: ** :	:*::** :	:*::** :
		ITAM	DOCK motif
hCLASP4	FEAPYTLGKKG	QGCIEEQCKRRT	ILTTSSNFPVKKRIPINCEQQINLKPIDGATDEIKD 1859
hCLASP5	YTTPTLEGRPR	GELHEQYRRNTV	LTMHAFPIKTRISVIOKEEFVLTPIEVAIEDMKK 1870
hCLASP3	YCTPFTLDGRA	HGELHEQFKRKT	ILTTSHAFPIKTRVNVTHKEEIIILTPIEVAIEDMQK 1992
hCLASP2	FEMPFTQTGKR	QGVVEEQCKRRT	ILTAIHCFPIVKKRIPVMYQHHTDLNPIEVAIDEMSK 1830
hCLASP7	FCTPFTPDGRA	HGELPEQHKRKT	LLSTDHAFPIKTRIRVCHREETVLTPEVAIEDMQK 1911
hCLASP1	FETPFTLSGK	KHGVAEQCKRRT	ILTTSHLFPVKKRIQVISQSSTELNPIEVAIDEMSR 2032
	:*:* :	:*:* :	:*:* :
		Coiled-coil	
hCLASP4	KTAELQKLCSS	TDVDMIQQLKLG	QVSVQVNAGPLAYARAFNLDSQASKYPPKKVSELK 1919
hCLASP5	KTLQLAVAINQ	EPDPAKMLQMV	LQGSVGATVNVQGPLEVAQVFLAEIPADPKLYRHHNKLK 1930
hCLASP3	KTQELAFATHQ	DPADPKMLQMV	LQGSVGTTVNVQGPLEVAQVFLSEIPSDPKLFRHHNKLK 2052
hCLASP2	KVAELRQLCSS	AEVDMIKLQKL	QGSVSVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLK 1890
hCLASP7	KTRELAFA	TEQDPPDAKML	QMVQGSVGPTVNVQGPLEVAQVFLAEIPEDPKLFRHHNKLK 1971
hCLASP1	KVSELNQLCT	MEEVDMISLQL	KLGSVSVKVNAGPMAYARAFLEETNAKKYPDNQVKLLK 2092
	*. : *	* ** : ** *	*. ** ** : *. ** :
		Coiled-coil	
hCLASP4	DMFRKFQACSI	ALELNERLIKED	QVEYHEGLKSNFRDMVKELSDIIEHQILQEDTMHSP 1979
hCLASP5	LCFKEFIMRC	GEAVEKNKRLIT	ADQREYQQELKKNYNKLKENLRPMIERKIPELYKPIFR 1990
hCLASP3	LCFKDFTKRC	EDALRKNKSLIG	PVQKEYQRELGLSSP----- 2090
hCLASP2	EVFRQFVEAC	QALAVNERLIKED	QLEYQEEMKANYREMAKELSEIMHEQICPLEEKTS- 1949
hCLASP7	LCFKDFCKKC	EDALRKNKALIG	PDQKEYHRELERNYCRLREALQPIILTQRLPQLMAPTP- 2030
hCLASP1	EIFRQFADAC	QALDVNERLIKED	QLEYQEELRSHYKDMLSELSTVMNEQITGRDDL SKR 2152
	:. *	*: ** *	* ** : *
		PDZ ligand	
hCLASP4	WMSNTLHVFC	AIISGTSSDRGY	GSPRYAEV--- 2008
hCLASP5	VESQKRDSF	HRRSFRKCETQ	LSQGS----- 2015
hCLASP3	-----	-----	-----
hCLASP2	VLPNSLHIF	NAISGTPSTMV	HGMTSSSSVV 1980
hCLASP7	---PGLRNSL	NRASFRKADL	----- 2047
hCLASP1	GVDQTCTRV	ISKATPALPTV	SISSSAEV--- 2180

FIG. 8 (6 of 6)